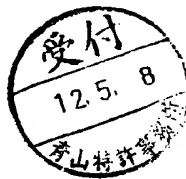


PATENT COOPERATION TREATY

From the:
INTERNATIONAL PRELIMINARY EXAMINING AUTHORITY

To:

AOYAMA, Tamotsu et al.
Aoyama & Partners
IMP Building, 3-7, Shiromi
1-chome, Chuo-ku, Osaka-shi
Osaka 540-0001
JAPON



PCT

WRITTEN OPINION

(PCT Rule 66)

Date of mailing (day/month/year) 02.05.2000	
Applicant's or agent's file reference 661102	REPLY DUE within 3 month(s) from the above date of mailing
International application No. PCT/JP99/03929	International filing date (day/month/year) 22/07/1999
Priority date (day/month/year) 24/07/1998	
International Patent Classification (IPC) or both national classification and IPC C12N15/12	
Applicant SAGAMI CHEMICAL RESEARCH CENTER et al.	

1. This written opinion is the **first** drawn up by this International Preliminary Examining Authority.
2. This opinion contains indications relating to the following items:
 - I ☒ Basis of the opinion
 - II ☐ Priority
 - III ☒ Non-establishment of opinion with regard to novelty, inventive step and industrial applicability
 - IV ☐ Lack of unity of invention
 - V ☒ Reasoned statement under Rule 66.2(a)(ii) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement
 - VI ☐ Certain document cited
 - VII ☐ Certain defects in the international application
 - VIII ☐ Certain observations on the international application
3. The applicant is hereby **invited to reply** to this opinion.

When? See the time limit indicated above. The applicant may, before the expiration of that time limit, request this Authority to grant an extension, see Rule 66.2(d).

How? By submitting a written reply, accompanied, where appropriate, by amendments, according to Rule 66.3. For the form and the language of the amendments, see Rules 66.8 and 66.9.

Also: For an additional opportunity to submit amendments, see Rule 66.4.
For the examiner's obligation to consider amendments and/or arguments, see Rule 66.4 bis.
For an informal communication with the examiner, see Rule 66.6.

If no reply is filed, the international preliminary examination report will be established on the basis of this opinion.
4. The final date by which the international preliminary examination report must be established according to Rule 69.2 is: 24/11/2000.

Name and mailing address of the international preliminary examining authority: European Patent Office D-80298 Munich Tel. +49 89 2399 - 0 Tx: 523656 epmu d Fax: +49 89 2399 - 4465	Authorized officer / Examiner Vollbach, S Formalities officer (incl. extension of time limits) Vullo, C Telephone No. +49 89 2399 8061
-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------	----------------------------------------------------------------------------------------------------------------------------------------------------



WRITTEN OPINION

International application No. PCT/JP99/03929

I. Basis of the opinion

1. This opinion has been drawn on the basis of *(substitute sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this opinion as "originally filed".)*:

Description, pages:

1-121 as originally filed

Claims, No.:

1-6 as originally filed

Drawings, sheets:

1/50-50/50 as originally filed

2. The amendments have resulted in the cancellation of:

- ☐ the description, pages:
- ☐ the claims, Nos.:
- ☐ the drawings, sheets:

3. This opinion has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed (Rule 70.2(c)):

4. Additional observations, if necessary:

III. Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

The questions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been and will not be examined in respect of:

- ☐ the entire international application,
- ☒ claims Nos. 1-6 partially,

because:

- ☐ the said international application, or the said claims Nos. relate to the following subject matter which does not require an international preliminary examination (*specify*):

WRITTEN OPINION

International application No. PCT/JP99/03929

- ☐ the description, claims or drawings (*indicate particular elements below*) or said claims Nos. are so unclear that no meaningful opinion could be formed (*specify*):
- ☐ the claims, or said claims Nos. are so inadequately supported by the description that no meaningful opinion could be formed.
- ☒ no international search report has been established for the said claims Nos. 1-6 partially.

V. Reasoned statement under Rule 66.2(a)(ii) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)	Claims
Inventive step (IS)	Claims 1-6
Industrial applicability (IA)	Claims

2. Citations and explanations

see separate sheet

1. The search authority raised an objection for lack of unity of the application. Since no required additional search fees were paid by the applicant, search has only been carried out on the invention first mentioned in the claims i.e. Seq. ID Nos 1,11 and 21. Examination can thus only be based on said subject-matter.

2. The present application relates to a protein having the amino acid sequence shown in Seq ID No 1, the cDNA shown in Seq. ID Nos 11 and 21, expression vectors comprising these sequences and transformed eucaryotic hosts.

The DNA sequences have been selected from cDNA libraries by the presence of a hydrophobic region being a putative secretory signal or transmembrane.

In particular the clone HP01550 (Seq. ID Nos 1,11, and 21) is a clone from a human stomach cancer cDNA library which consists of 65-bp 5'-untranslated region, a 378-bp ORF, and a 67-bp 3' untranslated region. The ORF codes for a protein of 125 amino acids and the expressed protein has a molecular weight of 15 kDa. Search in a protein data base revealed a similarity to the *Caenorhabditis elegans* hypothetical proteins F45G2.c and F45G2.c. In addition the search of the GenBank revealed an EST which shares more than 90% homology.

3. As far as patentability of the specific claimed sequences are concerned the following considerations apply:

The specific claimed sequences are new according to the requirements set out in Article 33(2) PCT.

However, an inventive step cannot be recognized because in general the provision of a DNA sequence without an indication of how to use said DNA sequence (specific technical purpose) is not inventive per se (Article 33(3) PCT). This also apply to the encoded protein even if expression has been carried out.

It should be noted, that all subject-matter which might involve a certain contribution to the art, namely the determination of the function of the protein and methods which make use of said protein and the encoding DNA sequence have not been carried out. Therefore an inventive step is not recognized by the present authority for claims 1-6 (Article 33(3) PCT).

PATENT COOPERATION TREATY

PCT

NOTIFICATION OF RECEIPT OF
RECORD COPY

(PCT Rule 24.2(a))



From the INTERNATIONAL BUREAU

To:

AOYAMA, Tamotsu
 AOYAMA & PARTNERS
 IMP Building
 3-7, Shiromi 1-chome, Chuo-ku
 Osaka-shi
 Osaka 540-0001
 JAPON

Date of mailing (day/month/year) 17 August 1999 (17.08.99)	IMPORTANT NOTIFICATION
Applicant's or agent's file reference 661102	International application No. PCT/JP99/03929

The applicant is hereby notified that the International Bureau has received the record copy of the international application as detailed below.

Name(s) of the applicant(s) and State(s) for which they are applicants:

SAGAMI CHEMICAL RESEARCH CENTER et al (for all designated States except US)
 KATO, Seishi et al (for US)

International filing date	:	22 July 1999 (22.07.99)
Priority date(s) claimed	:	24 July 1998 (24.07.98) 07 August 1998 (07.08.98) 25 August 1998 (25.08.98) 09 September 1998 (09.09.98) 29 September 1998 (29.09.98)

Date of receipt of the record copy by the International Bureau	:	06 August 1999 (06.08.99)
----------------------------------------------------------------	---	---------------------------

List of designated Offices	:	
----------------------------	---	--

AP : GH, GM, KE, LS, MW, SD, SZ, UG, ZW
 EA : AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
 EP : AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
 OA : BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
 National : AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE,
 GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO,
 NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW

The International Bureau of WIPO 34, chemin des Colombettes 1211 Geneva 20, Switzerland	Authorized officer: M. Sakai
Facsimile No. (41-22) 740.14.35	Telephone No. (41-22) 338.83.38

Continuation of Form PCT/IB/3

NOTIFICATION OF RECEIPT OF RECORD COPY

Date of mailing (day/month/year) 17 August 1999 (17.08.99)	IMPORTANT NOTIFICATION
Applicant's or agent's file reference 661102	International application No. PCT/JP99/03929

ATTENTION

The applicant should carefully check the data appearing in this Notification. In case of any discrepancy between these data and the indications in the international application, the applicant should immediately inform the International Bureau.

In addition, the applicant's attention is drawn to the information contained in the Annex, relating to:

- ☒ time limits for entry into the national phase
- ☒ confirmation of precautionary designations
- ☒ requirements regarding priority documents

A copy of this Notification is being sent to the receiving Office and to the International Searching Authority.

INFORMATION ON TIME LIMITS FOR ENTERING THE NATIONAL PHASE

The applicant is reminded that the "national phase" must be entered before each of the designated Offices indicated in the Notification of Receipt of Record Copy (Form PCT/IB/301) by paying national fees and furnishing translations, as prescribed by the applicable national laws.

The time limit for performing these procedural acts is **20 MONTHS** from the priority date or, for those designated States which the applicant elects in a demand for international preliminary examination or in a later election, **30 MONTHS** from the priority date, provided that the election is made before the expiration of 19 months from the priority date. Some designated (or elected) Offices have fixed time limits which expire even later than 20 or 30 months from the priority date. In other Offices an extension of time or grace period, in some cases upon payment of an additional fee, is available.

In addition to these procedural acts, the applicant may also have to comply with other special requirements applicable in certain Offices. It is the applicant's responsibility to ensure that the necessary steps to enter the national phase are taken in a timely fashion. Most designated Offices do not issue reminders to applicants in connection with the entry into the national phase.

For detailed information about the procedural acts to be performed to enter the national phase before each designated Office, the applicable time limits and possible extensions of time or grace periods, and any other requirements, see the relevant Chapters of Volume II of the PCT Applicant's Guide. Information about the requirements for filing a demand for international preliminary examination is set out in Chapter IX of Volume I of the PCT Applicant's Guide.

GR and ES became bound by PCT Chapter II on 7 September 1996 and 6 September 1997, respectively, and may, therefore, be elected in a demand or a later election filed on or after 7 September 1996 and 6 September 1997, respectively, regardless of the filing date of the international application. (See second paragraph above.)

Note that only an applicant who is a national or resident of a PCT Contracting State which is bound by Chapter II has the right to file a demand for international preliminary examination.

CONFIRMATION OF PRECAUTIONARY DESIGNATIONS

This notification lists only specific designations made under Rule 4.9(a) in the request. It is important to check that these designations are correct. Errors in designations can be corrected where precautionary designations have been made under Rule 4.9(b). The applicant is hereby reminded that any precautionary designations may be confirmed according to Rule 4.9(c) before the expiration of 15 months from the priority date. If it is not confirmed, it will automatically be regarded as withdrawn by the applicant. There will be no reminder and no invitation. Confirmation of a designation consists of the filing of a notice specifying the designated State concerned (with an indication of the kind of protection or treatment desired) and the payment of the designation and confirmation fees. Confirmation must reach the receiving Office within the 15-month time limit.

REQUIREMENTS REGARDING PRIORITY DOCUMENTS

For applicants who have not yet complied with the requirements regarding priority documents, the following is recalled.

Where the priority of an earlier national, regional or international application is claimed, the applicant must submit a copy of the said earlier application, certified by the authority with which it was filed ("the priority document") to the receiving Office (which will transmit it to the International Bureau) or directly to the International Bureau, before the expiration of 16 months from the priority date, provided that any such priority document may still be submitted to the International Bureau before that date of international publication of the international application, in which case that document will be considered to have been received by the International Bureau on the last day of the 16-month time limit (Rule 17.1(a)).

Where the priority document is issued by the receiving Office, the applicant may, instead of submitting the priority document, request the receiving Office to prepare and transmit the priority document to the International Bureau. Such request must be made before the expiration of the 16-month time limit and may be subjected by the receiving Office to the payment of a fee (Rule 17.1(b)).

If the priority document concerned is not submitted to the International Bureau or if the request to the receiving Office to prepare and transmit the priority document has not been made (and the corresponding fee, if any, paid) within the applicable time limit indicated under the preceding paragraphs, any designated State may disregard the priority claim, provided that no designated Office may disregard the priority claim concerned before giving the applicant an opportunity to furnish the priority document within a time limit which is reasonable under the circumstances.

Where several priorities are claimed, the priority date to be considered for the purposes of computing the 16-month time limit is the filing date of the earliest application whose priority is claimed.

PATENT COOPERATION TREATY

PCT

NOTIFICATION CONCERNING
SUBMISSION OR TRANSMITTAL
OF PRIORITY DOCUMENT

(PCT Administrative Instructions, Section 411)

From the INTERNATIONAL BUREAU

To:

AOYAMA, Tamotsu
AOYAMA & PARTNERS
IMP Building
3-7, Shiromi 1-chome, Chuo-ku
Osaka-shi
Osaka 540-0001
JAPON

Date of mailing (day/month/year)
06 October 1999 (06.10.99)

Applicant's or agent's file reference
661102

International application No.
PCT/JP99/03929

International publication date (day/month/year)
Not yet published

International filing date (day/month/year)
22 July 1999 (22.07.99)

Priority date (day/month/year)
24 July 1998 (24.07.98)

Applicant

SAGAMI CHEMICAL RESEARCH CENTER et al

IMPORTANT NOTIFICATION

1. The applicant is hereby notified of the date of receipt (except where the letters "NR" appear in the right-hand column) by the International Bureau of the priority document(s) relating to the earlier application(s) indicated below. Unless otherwise indicated by an asterisk appearing next to a date of receipt, or by the letters "NR", in the right-hand column, the priority document concerned was submitted or transmitted to the International Bureau in compliance with Rule 17.1(a) or (b).
2. This updates and replaces any previously issued notification concerning submission or transmittal of priority documents.
3. An asterisk(*) appearing next to a date of receipt, in the right-hand column, denotes a priority document submitted or transmitted to the International Bureau but not in compliance with Rule 17.1(a) or (b). In such a case, the attention of the applicant is directed to Rule 17.1(c) which provides that no designated Office may disregard the priority claim concerned before giving the applicant an opportunity, upon entry into the national phase, to furnish the priority document within a time limit which is reasonable under the circumstances.
4. The letters "NR" appearing in the right-hand column denote a priority document which was not received by the International Bureau or which the applicant did not request the receiving Office to prepare and transmit to the International Bureau, as provided by Rule 17.1(a) or (b), respectively. In such a case, the attention of the applicant is directed to Rule 17.1(c) which provides that no designated Office may disregard the priority claim concerned before giving the applicant an opportunity, upon entry into the national phase, to furnish the priority document within a time limit which is reasonable under the circumstances.

<u>Priority date</u>	<u>Priority application No.</u>	<u>Country or regional Office or PCT receiving Office</u>	<u>Date of receipt of priority document</u>
24 July 1998 (24.07.98)	10/208820	JP	27 Sept 1999 (27.09.99)

The International Bureau of WIPO
34, chemin des Colombettes
1211 Geneva 20, Switzerland

Facsimile No. (41-22) 740.14.35

Authorized officer

Juan Cruz

Telephone No. (41-22) 338.83.38

Form PCT/IB/304 (July 1998)

002881955

外国方式

PATENT COOPERATION TREATY

WO 00/05367
PCT/JP99/03929

PCT

NOTICE INFORMING THE APPLICANT OF THE COMMUNICATION OF THE INTERNATIONAL APPLICATION TO THE DESIGNATED OFFICES

(PCT Rule 47.1(c), first sentence)

From the INTERNATIONAL BUREAU

To:

AOYAMA, Tamotsu
Aoyama & Partners
IMP Building
3-7, Shiromi 1-chome, Chuo-ku
Osaka-shi
Osaka 540-0001
JAPON



Date of mailing (day/month/year) 03 February 2000 (03.02.00)		
Applicant's or agent's file reference 661102		IMPORTANT NOTICE
International application No. PCT/JP99/03929	International filing date (day/month/year) 22 July 1999 (22.07.99)	Priority date (day/month/year) 24 July 1998 (24.07.98)
Applicant SAGAMI CHEMICAL RESEARCH CENTER et al		

1. Notice is hereby given that the International Bureau has communicated, as provided in Article 20, the international application to the following designated Offices on the date indicated above as the date of mailing of this Notice:
AU,CN,EP,IL,JP,KR,US

In accordance with Rule 47.1(c), third sentence, those Offices will accept the present Notice as conclusive evidence that the communication of the international application has duly taken place on the date of mailing indicated above and no copy of the international application is required to be furnished by the applicant to the designated Office(s).

2. The following designated Offices have waived the requirement for such a communication at this time:
AE,AL,AM,AP,AT,AZ,BA,BB,BG,BR,BY,CA,CH,CU,CZ,DE,DK,EA,EE,ES,FI,GB,GD,GE,GH,GM,HR,
HU,ID,IN,IS,KE,KG,KZ,LC,LK,LR,LS,LT,LU,LV,MD,MG,MK,MN,MW,MX,NO,NZ,OA,PL,PT,RO,RU,
SD,SE,SG,SI,SK,SL,TJ,TM,TR,TT,UA,UG,UZ,VN,YU,ZA,ZW
The communication will be made to those Offices only upon their request. Furthermore, those Offices do not require the applicant to furnish a copy of the international application (Rule 49.1(a-bis)).
3. Enclosed with this Notice is a copy of the international application as published by the International Bureau on
03 February 2000 (03.02.00) under No. WO 00/05367

REMINDER REGARDING CHAPTER II (Article 31(2)(a) and Rule 54.2)

If the applicant wishes to postpone entry into the national phase until 30 months (or later in some Offices) from the priority date, a demand for international preliminary examination must be filed with the competent International Preliminary Examining Authority before the expiration of 19 months from the priority date.

It is the applicant's sole responsibility to monitor the 19-month time limit.

Note that only an applicant who is a national or resident of a PCT Contracting State which is bound by Chapter II has the right to file a demand for international preliminary examination.

REMINDER REGARDING ENTRY INTO THE NATIONAL PHASE (Article 22 or 39(1))

If the applicant wishes to proceed with the international application in the national phase, he must, within 20 months or 30 months, or later in some Offices, perform the acts referred to therein before each designated or elected Office.

For further important information on the time limits and acts to be performed for entering the national phase, see the Annex to Form PCT/IB/301 (Notification of Receipt of Record Copy) and Volume II of the PCT Applicant's Guide.

The International Bureau of WIPO 34, chemin des Colombettes 1211 Geneva 20, Switzerland	Authorized officer J. Zahra
Facsimile No. (41-22) 740.14.35	Telephone No. (41-22) 338.83.38

PATENT COOPERATION TREATY

PCT

INFORMATION CONCERNING ELECTED
OFFICES NOTIFIED OF THEIR ELECTION

(PCT Rule 61.3)

From the INTERNATIONAL BUREAU

To:

AOYAMA, Tamotsu
Aoyama & Partners
IMP Building
3-7, Shiromi 1-chome, Chuo-ku
Osaka-shi
Osaka 540-0001
JAPON

Date of mailing (day/month/year)
01 March 2000 (01.03.00)

Applicant's or agent's file reference
661102

IMPORTANT INFORMATION

International application No.
PCT/JP99/03929

International filing date (day/month/year)
22 July 1999 (22.07.99)

Priority date (day/month/year)
24 July 1998 (24.07.98)

Applicant
SAGAMI CHEMICAL RESEARCH CENTER et al

1. The applicant is hereby informed that the International Bureau has, according to Article 31(7), notified each of the following Offices of its election:

AP : GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW

EP : AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

National : AU, BG, BR, CA, CN, CZ, DE, IL, JP, KR, MN, NO, NZ, PL, RO, RU, SE, SK, US

2. The following Offices have waived the requirement for the notification of their election; the notification will be sent to them by the International Bureau only upon their request:

EA : AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

OA : BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

National : AE, AL, AM, AT, AZ, BA, BB, BY, CH, CU, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IN, IS, KE, KG, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MW, MX, PT, SD, SG, SI, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW

3. The applicant is reminded that he must enter the "national phase" before the expiration of 30 months from the priority date before each of the Offices listed above. This must be done by paying the national fee(s) and furnishing, if prescribed, a translation of the international application (Article 39(1)(a)), as well as, where applicable, by furnishing a translation of any annexes of the international preliminary examination report (Article 36(3)(b) and Rule 74.1).

Some offices have fixed time limits expiring later than the above-mentioned time limit. For detailed information about the applicable time limits and the acts to be performed upon entry into the national phase before a particular Office, see Volume II of the PCT Applicant's Guide.

The entry into the European regional phase is postponed until 31 months from the priority date for all States designated for the purposes of obtaining a European patent.

The International Bureau of WIPO
34, chemin des Colombettes
1211 Geneva 20, Switzerland

Facsimile No. (41-22) 740.14.35

Authorized officer:

R. Forax

Telephone No. (41-22) 338.83.38

3136756

From the
INTERNATIONAL PRELIMINARY EXAMINING AUTHORITY

PCT

To:

AOYAMA, Tamotsu et al.
Aoyama & Partners
IMP Building, 3-7, Shiromi
1-chome, Chuo-ku, Osaka-shi
Osaka 540-0001
JAPON



**NOTIFICATION OF RECEIPT
OF DEMAND BY COMPETENT INTERNATIONAL
PRELIMINARY EXAMINING AUTHORITY**

(PCT Rules 59.3(e) and 61.1(b), first sentence
and Administrative Instructions, Section 601(a))

Date of mailing
(day/month/year)

18. 02. 00

Applicant's or agent's file reference
661102

IMPORTANT NOTIFICATION

International application No.

PCT/ JP 99/ 03929

International filing date (day/month/year)

22/07/1999

Priority date (day/month/year)

24/07/1998

Applicant

SAGAMI CHEMICAL RESEARCH CENTER et al.

1. The applicant is hereby notified that this International Preliminary Examining Authority considers the following date as the date of receipt of the demand for international preliminary examination of the international application:

03/02/2000

2. This date of receipt is:



the actual date of receipt of the demand by this Authority (Rule 61.1(b)).



the actual date of receipt of the demand on behalf of this Authority (Rule 59.3(e)).



the date on which this Authority has, in response to the invitation to correct defects in the demand (Form PCT/IPEA/404), received the required corrections.

3. ☐ **ATTENTION:** That date of receipt is **AFTER** the expiration of 19 months from the priority date. Consequently, the election(s) made in the demand does (do) not have the effect of postponing the entry into the national phase until 30 months from the priority date (or later in some Offices) (Article 39(1)). Therefore, the acts for entry into the national phase must be performed within 20 months from the priority date (or later in some Offices) (Article 22). For details, see the *PCT Applicant's Guide*, Volume II.



(If applicable) This notification confirms the information given by telephone, facsimile transmission or in person on:

4. Only where paragraph 3 applies, a copy of this notification has been sent to the International Bureau.

Name and mailing address of the IPEA/



European Patent Office
D-80298 Munich
Tel. (+49-89) 2399-0, Tx: 523656 epmu d
Fax: (+49-89) 2399-4465

Authorized officer

DANISSEN P T

Tel. (+49-89) 2399-8862



REC'D 15 NOV 2000

WIPO PCT

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference 661102	FOR FURTHER ACTION See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416)	
International application No. PCT/JP99/03929	International filing date (day/month/year) 22/07/1999	Priority date (day/month/year) 24/07/1998
International Patent Classification (IPC) or national classification and IPC C12N15/12		
Applicant SAGAMI CHEMICAL RESEARCH CENTER et al.		

1. This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.



2. This REPORT consists of a total of 5 sheets, including this cover sheet.

- ☐ This report is also accompanied by ANNEXES, i.e. sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).

These annexes consist of a total of sheets.

3. This report contains indications relating to the following items:

- I ☒ Basis of the report
- II ☐ Priority
- III ☒ Non-establishment of opinion with regard to novelty, inventive step and industrial applicability
- IV ☐ Lack of unity of invention
- V ☒ Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement
- VI ☐ Certain documents cited
- VII ☐ Certain defects in the international application
- VIII ☐ Certain observations on the international application

Date of submission of the demand 03/02/2000	Date of completion of this report 13.11.2000
Name and mailing address of the international preliminary examining authority:  European Patent Office D-80298 Munich Tel. +49 89 2399 - 0 Tx: 523656 epmu d Fax: +49 89 2399 - 4465	Authorized officer Vollbach, S Telephone No. +49 89 2399 8715 

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No. PCT/JP99/03929

I. Basis of the report

1. This report has been drawn on the basis of *(substitute sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to the report since they do not contain amendments (Rules 70.16 and 70.17).):*

Description, pages:

1-121 as originally filed

Claims, No.:

1-6 as originally filed

Drawings, sheets:

1/50-50/50 as originally filed

2. With regard to the **language**, all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.

These elements were available or furnished to this Authority in the following language: , which is:

- ☐ the language of a translation furnished for the purposes of the international search (under Rule 23.1(b)).
- ☐ the language of publication of the international application (under Rule 48.3(b)).
- ☐ the language of a translation furnished for the purposes of international preliminary examination (under Rule 55.2 and/or 55.3).

3. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international preliminary examination was carried out on the basis of the sequence listing:

- ☐ contained in the international application in written form.
- ☐ filed together with the international application in computer readable form.
- ☐ furnished subsequently to this Authority in written form.
- ☐ furnished subsequently to this Authority in computer readable form.
- ☐ The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.
- ☐ The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

4. The amendments have resulted in the cancellation of:

- ☐ the description, pages:
- ☐ the claims, Nos.:

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT**

International application No. PCT/JP99/03929

☐ the drawings, sheets:

5. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed (Rule 70.2(c)):

(Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report.)

6. Additional observations, if necessary:

III. Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

The questions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been examined in respect of:

☐ the entire international application.

☒ claims Nos. 1-6 partially.

because:

☐ the said international application, or the said claims Nos. relate to the following subject matter which does not require an international preliminary examination (*specify*):

☐ the description, claims or drawings (*indicate particular elements below*) or said claims Nos. are so unclear that no meaningful opinion could be formed (*specify*):

☐ the claims, or said claims Nos. are so inadequately supported by the description that no meaningful opinion could be formed.

☒ no international search report has been established for the said claims Nos. 1-6 partially.

2. A meaningful international preliminary examination report cannot be carried out due to the failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions:

☐ the written form has not been furnished or does not comply with the standard.

☐ the computer readable form has not been furnished or does not comply with the standard.

V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)

Yes: Claims 1-6

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT**

International application No. PCT/JP99/03929

	No:	Claims	
Inventive step (IS)	Yes:	Claims	
	No:	Claims	1-6
Industrial applicability (IA)	Yes:	Claims	
	No:	Claims	1-6

2. Citations and explanations
see separate sheet

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT - SEPARATE SHEET**

International application No. PCT/JP99/03929

1. The search authority raised an objection for lack of unity of the application. Since no required additional search fees were paid by the applicant, search has only been carried out on the invention first mentioned in the claims i.e. Seq. ID Nos 1,11 and 21. Examination can thus only be based on said subject-matter.

2. The present application relates to a protein having the amino acid sequence shown in Seq ID No 1, the cDNA shown in Seq. ID Nos 11 and 21, expression vectors comprising these sequences and transformed eucaryotic hosts.

The DNA sequences have been selected from cDNA libraries by the presence of a hydrophobic region being a putative secretory signal or transmembrane.

In particular the clone HP01550 (Seq. ID Nos 1,11, and 21) is a clone from a human stomach cancer cDNA library which consists of 65-bp 5'-untranslated region, a 378-bp ORF, and a 67-bp 3' untranslated region. The ORF codes for a protein of 125 amino acids and the expressed protein has a molecular weight of 15 kDa. Search in a protein data base revealed a similarity to the *Caenorhabditis elegans* hypothetical proteins F45G2.c and F45G2.c. In addition the search of the GenBank revealed an EST which shares more than 90% homology.

3. As far as patentability of the specific claimed sequences are concerned the following considerations apply:

The specific claimed sequences are new according to the requirements set out in Article 33(2) PCT.

However, an inventive step cannot be recognized because in general the provision of a DNA sequence without an indication of how to use said DNA sequence (specific technical purpose) is not inventive per se (Article 33(3) PCT) and cannot be regarded as industrial applicable. This also apply to the encoded protein even if expression has been carried out.

It should be noted, that any subject-matter which might involve a certain contribution to the art, namely the determination of the function of the protein and methods which make use of said protein and the encoding DNA sequence have not been carried out. Therefore an inventive step is not recognized by the present authority for claims 1-6 (Article 33(3) PCT).

From the
INTERNATIONAL PRELIMINARY EXAMINING AUTHORITY

To:

AOYAMA, Tamotsu et al.
Aoyama & Partners
IMP Building, 3-7, Shiromi
1-chome, Chuo-ku, Osaka-shi
Osaka 540-0001
JAPON



PCT

NOTIFICATION OF TRANSMITTAL OF
THE INTERNATIONAL PRELIMINARY
EXAMINATION REPORT
(PCT Rule 71.1)

Date of mailing
(day/month/year) 13.11.2000

Applicant's or agent's file reference
661102

IMPORTANT NOTIFICATION

International application No.
PCT/JP99/03929

International filing date (day/month/year)
22/07/1999

Priority date (day/month/year)
24/07/1998

Applicant
SAGAMI CHEMICAL RESEARCH CENTER et al.

1. The applicant is hereby notified that this International Preliminary Examining Authority transmits herewith the international preliminary examination report and its annexes, if any, established on the international application.
2. A copy of the report and its annexes, if any, is being transmitted to the International Bureau for communication to all the elected Offices.
3. Where required by any of the elected Offices, the International Bureau will prepare an English translation of the report (but not of any annexes) and will transmit such translation to those Offices.

4. REMINDER

The applicant must enter the national phase before each elected Office by performing certain acts (filing translations and paying national fees) within 30 months from the priority date (or later in some Offices) (Article 39(1)) (see also the reminder sent by the International Bureau with Form PCT/IB/301).

Where a translation of the international application must be furnished to an elected Office, that translation must contain a translation of any annexes to the international preliminary examination report. It is the applicant's responsibility to prepare and furnish such translation directly to each elected Office concerned.

For further details on the applicable time limits and requirements of the elected Offices, see Volume II of the PCT Applicant's Guide.

Name and mailing address of the IPEA/

 European Patent Office
D-80298 Munich
Tel. +49 89 2399 - 0 Tx: 523656 epmu d
Fax: +49 89 2399 - 4465

Authorized officer

Emslander, S

Tel. +49 89 2399-8718





PATENT COOPERATION TREATY

PCT

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference 661102		See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416) FOR FURTHER ACTION	
International application No. PCT/JP99/03929	International filing date (day/month/year) 22/07/1999	Priority date (day/month/year) 24/07/1998	
International Patent Classification (IPC) or national classification and IPC C12N15/12			
Applicant SAGAMI CHEMICAL RESEARCH CENTER et al.			
<p>1. This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.</p> <p>2. This REPORT consists of a total of 5 sheets, including this cover sheet.</p> <p><input type="checkbox"/> This report is also accompanied by ANNEXES, i.e. sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).</p> <p>These annexes consist of a total of sheets.</p>			
<p>3. This report contains indications relating to the following items:</p> <ul style="list-style-type: none"> I <input checked="" type="checkbox"/> Basis of the report II <input type="checkbox"/> Priority III <input checked="" type="checkbox"/> Non-establishment of opinion with regard to novelty, inventive step and industrial applicability IV <input type="checkbox"/> Lack of unity of invention V <input checked="" type="checkbox"/> Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement VI <input type="checkbox"/> Certain documents cited VII <input type="checkbox"/> Certain defects in the international application VIII <input type="checkbox"/> Certain observations on the international application 			
Date of submission of the demand 03/02/2000		Date of completion of this report 13.11.2000	
Name and mailing address of the international preliminary examining authority:  European Patent Office D-80298 Munich Tel. +49 89 2399 - 0 Tx: 523656 epmu d Fax: +49 89 2399 - 4465		Authorized officer Vollbach, S Telephone No. +49 89 2399 8715 	

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT**

International application No. PCT/JP99/03929

I. Basis of the report

1. This report has been drawn on the basis of *(substitute sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to the report since they do not contain amendments (Rules 70.16 and 70.17).)*:

Description, pages:

1-121 as originally filed

Claims, No.:

1-6 as originally filed

Drawings, sheets:

1/50-50/50 as originally filed

2. With regard to the **language**, all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.

These elements were available or furnished to this Authority in the following language: , which is:

- ☐ the language of a translation furnished for the purposes of the international search (under Rule 23.1(b)).
- ☐ the language of publication of the international application (under Rule 48.3(b)).
- ☐ the language of a translation furnished for the purposes of international preliminary examination (under Rule 55.2 and/or 55.3).

3. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international preliminary examination was carried out on the basis of the sequence listing:

- ☐ contained in the international application in written form.
- ☐ filed together with the international application in computer readable form.
- ☐ furnished subsequently to this Authority in written form.
- ☐ furnished subsequently to this Authority in computer readable form.
- ☐ The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.
- ☐ The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

4. The amendments have resulted in the cancellation of:

- ☐ the description, pages:
- ☐ the claims, Nos.:

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT**

International application No. PCT/JP99/03929

☐ the drawings, sheets:

5. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed (Rule 70.2(c)):

(Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report.)

6. Additional observations, if necessary:

III. Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

The questions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been examined in respect of:

☐ the entire international application.

☒ claims Nos. 1-6 partially.

because:

☐ the said international application, or the said claims Nos. relate to the following subject matter which does not require an international preliminary examination (*specify*):

☐ the description, claims or drawings (*indicate particular elements below*) or said claims Nos. are so unclear that no meaningful opinion could be formed (*specify*):

☐ the claims, or said claims Nos. are so inadequately supported by the description that no meaningful opinion could be formed.

☒ no international search report has been established for the said claims Nos. 1-6 partially.

2. A meaningful international preliminary examination report cannot be carried out due to the failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions:

☐ the written form has not been furnished or does not comply with the standard.

☐ the computer readable form has not been furnished or does not comply with the standard.

V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)

Yes: Claims 1-6

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT**

International application No. PCT/JP99/03929

	No:	Claims	
Inventive step (IS)	Yes:	Claims	
	No:	Claims	1-6
Industrial applicability (IA)	Yes:	Claims	
	No:	Claims	1-6

2. Citations and explanations
see separate sheet

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT - SEPARATE SHEET**

International application No. PCT/JP99/03929

1. The search authority raised an objection for lack of unity of the application. Since no required additional search fees were paid by the applicant, search has only been carried out on the invention first mentioned in the claims i.e. Seq. ID Nos 1,11 and 21. Examination can thus only be based on said subject-matter.

2. The present application relates to a protein having the amino acid sequence shown in Seq ID No 1, the cDNA shown in Seq. ID Nos 11 and 21, expression vectors comprising these sequences and transformed eucaryotic hosts.

The DNA sequences have been selected from cDNA libraries by the presence of a hydrophobic region being a putative secretory signal or transmembrane.

In particular the clone HP01550 (Seq. ID Nos 1,11, and 21) is a clone from a human stomach cancer cDNA library which consists of 65-bp 5'-untranslated region, a 378-bp ORF, and a 67-bp 3' untranslated region. The ORF codes for a protein of 125 amino acids and the expressed protein has a molecular weight of 15 kDa. Search in a protein data base revealed a similarity to the *Caenorhabditis elegans* hypothetical proteins F45G2.c and F45G2.c. In addition the search of the GenBank revealed an EST which shares more than 90% homology.

3. As far as patentability of the specific claimed sequences are concerned the following considerations apply:

The specific claimed sequences are new according to the requirements set out in Article 33(2) PCT.

However, an inventive step cannot be recognized because in general the provision of a DNA sequence without an indication of how to use said DNA sequence (specific technical purpose) is not inventive per se (Article 33(3) PCT) and cannot be regarded as industrial applicable. This also apply to the encoded protein even if expression has been carried out.

It should be noted, that any subject-matter which might involve a certain contribution to the art, namely the determination of the function of the protein and methods which make use of said protein and the encoding DNA sequence have not been carried out. Therefore an inventive step is not recognized by the present authority for claims 1-6 (Article 33(3) PCT).

PCT REQUEST

Original (for SUBMISSION) - printed on 16.07.1999 10:35:27 AM

0	For receiving Office use only	
0-1	International Application No.	
0-2	International Filing Date	
0-3	Name of receiving Office and "PCT International Application"	
0-4	Form - PCT/RO/101 PCT Request	
0-4-1	Prepared using	PCT-EASY Version 2.84 (updated 01.07.1999)
0-5	Petition The undersigned requests that the present international application be processed according to the Patent Cooperation Treaty	
0-6	Receiving Office (specified by the applicant)	Japanese Patent Office (RO/JP)
0-7	Applicant's or agent's file reference	661102
I	Title of invention	HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS
II	Applicant	
II-1	This person is:	applicant only
II-2	Applicant for	all designated States except US
II-4	Name	SAGAMI CHEMICAL RESEARCH CENTER
II-5	Address:	4-1, Nishi-Ohnuma 4-chome, Sagamihara-shi, Kanagawa 229-0012 Japan
II-6	State of nationality	JP
II-7	State of residence	JP
III-1	Applicant and/or inventor	
III-1-1	This person is:	applicant only
III-1-2	Applicant for	all designated States except US
III-1-4	Name	PROTEGENE INC.
III-1-5	Address:	2-20-3, Naka-cho, Meguro-ku, Tokyo 153-0065 Japan
III-1-6	State of nationality	JP
III-1-7	State of residence	JP



PCT REQUEST

Original (for SUBMISSION) - printed on 16.07.1999 10:35:27 AM

III-2	Applicant and/or inventor	applicant and inventor US only KATO, Seishi 3-46-50, Wakamatsu, Sagamihara-shi, Kanagawa 229-0014 Japan JP JP
III-2-1	This person is:	
III-2-2	Applicant for	
III-2-4	Name (LAST, First)	
III-2-5	Address:	
III-2-6	State of nationality	
III-2-7	State of residence	
III-3	Applicant and/or inventor	applicant and inventor US only KIMURA, Tomoko 302, 4-1-28, Nishiikuta, Tama-ku, Kawasaki-shi, Kanagawa 214-0037 Japan JP JP
III-3-1	This person is:	
III-3-2	Applicant for	
III-3-4	Name (LAST, First)	
III-3-5	Address:	
III-3-6	State of nationality	
III-3-7	State of residence	
IV-1	Agent or common representative; or address for correspondence The person identified below is hereby/has been appointed to act on behalf of the applicant(s) before the competent International Authorities as:	agent AOYAMA, Tamotsu AOYAMA & PARTNERS IMP Building, 3-7, Shiromi 1-chome, chuo-ku, Osaka-shi, Osaka 540-0001 Japan (06) 6949-1261 (06) 6949-0361
IV-1-1	Name (LAST, First)	
IV-1-2	Address:	
IV-1-3	Telephone No.	
IV-1-4	Facsimile No.	
IV-2	Additional agent(s)	
IV-2-1	Name(s)	

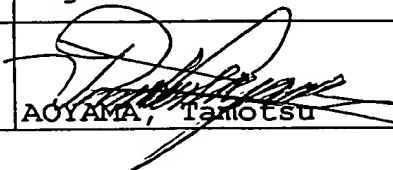
PCT REQUEST

Original (for SUBMISSION) - printed on 16.07.1999 10:35:27 AM

V V-1	Designation of States	
	Regional Patent (other kinds of protection or treatment, if any, are specified between parentheses after the designation(s) concerned)	<p>AP: GH GM KE LS MW SD SZ UG ZW and any other State which is a Contracting State of the Harare Protocol and of the PCT</p> <p>EA: AM AZ BY KG KZ MD RU TJ TM and any other State which is a Contracting State of the Eurasian Patent Convention and of the PCT</p> <p>EP: AT BE CH&LI CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE and any other State which is a Contracting State of the European Patent Convention and of the PCT</p> <p>OA: BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG and any other State which is a member State of OAPI and a Contracting State of the PCT</p>
V-2	National Patent (other kinds of protection or treatment, if any, are specified between parentheses after the designation(s) concerned)	<p>AE AL AM AT AU AZ BA BB BG BR BY CA CH&LI CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW</p>
V-5	Precautionary Designation Statement In addition to the designations made under items V-1, V-2 and V-3, the applicant also makes under Rule 4.9(b) all designations which would be permitted under the PCT except any designation(s) of the State(s) indicated under item V-6 below. The applicant declares that those additional designations are subject to confirmation and that any designation which is not confirmed before the expiration of 15 months from the priority date is to be regarded as withdrawn by the applicant at the expiration of that time limit.	
V-6	Exclusion(s) from precautionary designations	NONE
VI-1 VI-1-1 VI-1-2 VI-1-3	Priority claim of earlier national application Filing date Number Country	<p>24 July 1998 (24.07.1998)</p> <p>Patent Application No. 10-208820</p> <p>JP</p>
VI-2 VI-2-1 VI-2-2 VI-2-3	Priority claim of earlier national application Filing date Number Country	<p>07 August 1998 (07.08.1998)</p> <p>Patent Application No. 10-224105</p> <p>JP</p>

PCT REQUEST

Original (for SUBMISSION) - printed on 16.07.1999 10:35:27 AM

VI-3	Priority claim of earlier national application		
VI-3-1	Filing date	25 August 1998 (25.08.1998)	
VI-3-2	Number	Patent Application No. 10-238116	
VI-3-3	Country	JP	
VI-4	Priority claim of earlier national application		
VI-4-1	Filing date	09 September 1998 (09.09.1998)	
VI-4-2	Number	Patent Application No. 10-254736	
VI-4-3	Country	JP	
VI-5	Priority claim of earlier national application		
VI-5-1	Filing date	29 September 1998 (29.09.1998)	
VI-5-2	Number	Patent Application No. 10-275505	
VI-5-3	Country	JP	
VII-1	International Searching Authority Chosen	European Patent Office (EPO) (ISA/EP)	
VIII	Check list	number of sheets	electronic file(s) attached
VIII-1	Request	5	-
VIII-2	Description (excluding sequence listing part)	121	-
VIII-3	Claims	1	-
VIII-4	Abstract	1	661102.txt
VIII-5	Drawings	50	-
VIII-6	Sequence listing part of description	177	-
VIII-7	TOTAL	355	
	Accompanying items	paper document(s) attached	electronic file(s) attached
VIII-8	Fee calculation sheet	✓	-
VIII-9	Separate signed power of attorney	✓	-
VIII-15	Nucleotide and/or amino acid sequence listing in computer readable form		separate diskette
VIII-16	PCT-EASY diskette	-	diskette
VIII-17	Other (specified):	Revenue stamps of transmittal fee for receiving office	-
VIII-17	Other (specified):	Certificate of payment of basic & designation fee for International Bureau	-
VIII-17	Other (specified):	Certificate of payment of search fee for EPO	-
VIII-18	Figure of the drawings which should accompany the abstract		
VIII-19	Language of filing of the international application	English	
IX-1	Signature of applicant or agent		
IX-1-1	Name (LAST, First)	AOYAMA, Tamiotsu	

PCT REQUEST

661102

Original (for SUBMISSION) - printed on 16.07.1999 10:35:27 AM

FOR RECEIVING OFFICE USE ONLY

10-1	Date of actual receipt of the purported international application	
10-2	Drawings:	
10-2-1	Received	
10-2-2	Not received	
10-3	Corrected date of actual receipt due to later but timely received papers or drawings completing the purported international application	
10-4	Date of timely receipt of the required corrections under PCT Article 11(2)	
10-5	International Searching Authority	ISA/EP
10-6	Transmittal of search copy delayed until search fee is paid	

FOR INTERNATIONAL BUREAU USE ONLY

11-1	Date of receipt of the record copy by the International Bureau	
------	----------------------------------------------------------------	--

PCT (ANNEX - FEE CALCULATION SHEET)

661102

Original (for SUBMISSION) - printed on 16.07.1999 10:35:27 AM

(This sheet is not part of and does not count as a sheet of the international application)

0	For receiving Office use only	
0-1	International Application No.	
0-2	Date stamp of the receiving Office	
0-4	Form - PCT/RO/101 (Annex) PCT Fee Calculation Sheet	
0-4-1	Prepared using	PCT-EASY Version 2.84 (updated 01.07.1999)
0-9	Applicant's or agent's file reference	661102
2	Applicant	SAGAMI CHEMICAL RESEARCH CENTER, et al.
12	Calculation of prescribed fees	fee amount/multiplier total amounts (JPY)
12-1	Transmittal fee T	⇒ 18,000
12-2	Search fee S	⇒ 120,000
12-3	International fee Basic fee (first 30 sheets) b1	54,800
12-4	Remaining sheets	325
12-5	Additional amount (X)	1,300
12-6	Total additional amount b2	422,500
12-7	b1 + b2 = B	477,300
12-8	Designation fees Number of designations contained in international application	78
12-9	Number of designation fees payable (maximum 10)	10
12-10	Amount of designation fee (X)	12,600
12-11	Total designation fees D	126,000
12-12	PCT-EASY fee reduction R	-16,900
12-13	Total International fee (B+D-R) I	⇒ 586,400
12-17	TOTAL FEES PAYABLE (T+S+I+P)	⇒ 724,400
12-19	Mode of payment	Transmittal fee: revenue stamps Search fee: bank draft International fee: bank draft Priority document fee: revenue stamps

VALIDATION LOG AND REMARKS

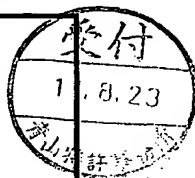
13-1-1	Applicant remarks Names	6214 Patent Attorney AOYAMA Tamotsu 6852 Patent Attorney TAMURA Yasuo 6703 Patent Attorney IWASAKI Mitsutaka
13-2-1	Validation messages Request	Green? The title of the invention should preferably be entered in capital letters. Please verify.

From the INTERNATIONAL SEARCHING AUTHORITY

PCT

To:

Aoyama & Partners
Attn. AOYAMA, T
IMP Building, 3-7, Shiromi
1-chome, Chuo-ku, Osaka-shi
Osaka 540-0001
JAPAN

NOTIFICATION OF RECEIPT
OF SEARCH COPY

(PCT Rule 25.1)

Date of mailing
(day/month/year)

20/08/1999

Applicant's or agent's file reference

661102

IMPORTANT NOTIFICATION

International application No.

PCT/JP 99/03929

International filing date(day/month/year)

22/07/1999

Priority date (day/month/year)

24/07/1998

Applicant

SAGAMI CHEMICAL RESEARCH CENTER et al.

1. Where the International Searching Authority and the Receiving Office are not the same office:

The applicant is hereby notified that the search copy of the international application was received by this International Searching Authority on the date indicated below.

Where the International Searching Authority and the Receiving Office are the same office:

The applicant is hereby notified that the search copy of the international application was received on the date indicated below.

05/08/1999 (date of receipt).

2. ☐ The search copy was accompanied by a nucleotide and/or amino acid sequence listing in computer readable form.

3. Time limit for establishment of International Search Report

The applicant is informed that the time limit for establishing the International Search Report is 3 months from the date of receipt indicated above or 9 months from the priority date, whichever time limit expires later

4. A copy of this notification has been sent to the International Bureau and, where the first sentence of paragraph 1 applies, to the Receiving Office.

Name and mailing address of the International Searching Authority



European Patent Office, P.B. 5818 Patentlaan 2
NL-2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl
Fax: (+31-70) 340-3016

Authorized officer

ISA/EP

PATENT COOPERATION T

PCT

NOTIFICATION OF ELECTION

(PCT Rule 61.2)

From the INTERNATIONAL BUREAU

To:

Assistant Commissioner for Patents
United States Patent and Trademark
Office
Box PCT
Washington, D.C.20231
ÉTATS-UNIS D'AMÉRIQUE

in its capacity as elected Office

Date of mailing (day/month/year) 01 March 2000 (01.03.00)	
International application No. PCT/JP99/03929	Applicant's or agent's file reference 661102
International filing date (day/month/year) 22 July 1999 (22.07.99)	Priority date (day/month/year) 24 July 1998 (24.07.98)
Applicant KATO, Seishi et al	

1. The designated Office is hereby notified of its election made:

☒ in the demand filed with the International Preliminary Examining Authority on:

03 February 2000 (03.02.00)

☐ in a notice effecting later election filed with the International Bureau on:
2. The election ☒ was
☐ was not

made before the expiration of 19 months from the priority date or, where Rule 32 applies, within the time limit under Rule 32.2(b).

The International Bureau of WIPO
34, chemin des Colombettes
1211 Geneva 20, Switzerland

Authorized officer

R. Forax

Facsimile No.: (41-22) 740.14.35

Telephone No.: (41-22) 338.83.38

From the INTERNATIONAL SEARCHING AUTHORITY

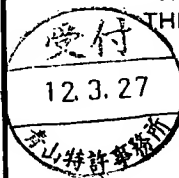
PCT

To:

Aoyama & Partners
Attn. AOYAMA, T
IMP Building, 3-7, Shiromi
1-chome, Chuo-ku, Osaka-shi
Osaka 540-0001
JAPAN

NOTIFICATION OF TRANSMITTAL OF
THE INTERNATIONAL SEARCH REPORT
OR THE DECLARATION

(PCT Rule 44.1)



Date of mailing
(day/month/year)

06/03/2000

Applicant's or agent's file reference

661102

FOR FURTHER ACTION

See paragraphs 1 and 4 below

International application No.

PCT/JP 99/03929

International filing date

(day/month/year)

22/07/1999

Applicant

SAGAMI CHEMICAL RESEARCH CENTER et al.

1. ☒ The applicant is hereby notified that the International Search Report has been established and is transmitted herewith.

Filing of amendments and statement under Article 19:

The applicant is entitled, if he so wishes, to amend the claims of the International Application (see Rule 46):

When? The time limit for filing such amendments is normally 2 months from the date of transmittal of the International Search Report; however, for more details, see the notes on the accompanying sheet.

Where? Directly to the International Bureau of WIPO
34, chemin des Colombettes
1211 Geneva 20, Switzerland
Facsimile No.: (41-22) 740.14.35

For more detailed instructions, see the notes on the accompanying sheet.

2. ☐ The applicant is hereby notified that no International Search Report will be established and that the declaration under Article 17(2)(a) to that effect is transmitted herewith.

3. ☐ With regard to the protest against payment of (an) additional fee(s) under Rule 40.2, the applicant is notified that:

☐ the protest together with the decision thereon has been transmitted to the International Bureau together with the applicant's request to forward the texts of both the protest and the decision thereon to the designated Offices.

☐ no decision has been made yet on the protest; the applicant will be notified as soon as a decision is made.

4. **Further action(s):** The applicant is reminded of the following:

Shortly after **18 months** from the priority date, the international application will be published by the International Bureau. If the applicant wishes to avoid or postpone publication, a notice of withdrawal of the international application, or of the priority claim, must reach the International Bureau as provided in Rules 90bis.1 and 90bis.3, respectively, before the completion of the technical preparations for international publication.

Within **19 months** from the priority date, a demand for international preliminary examination must be filed if the applicant wishes to postpone the entry into the national phase until 30 months from the priority date (in some Offices even later).

Within **20 months** from the priority date, the applicant must perform the prescribed acts for entry into the national phase before all designated Offices which have not been elected in the demand or in a later election within 19 months from the priority date or could not be elected because they are not bound by Chapter II.

Name and mailing address of the International Searching Authority



European Patent Office, P.B. 5818 Patentlaan 2
NL-2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Mireille Claudepierre

NOTES TO FORM PCT/ISA/220

These Notes are intended to give the basic instructions concerning the filing of amendments under article 19. The Notes are based on the requirements of the Patent Cooperation Treaty, the Regulations and the Administrative Instructions under that Treaty. In case of discrepancy between these Notes and those requirements, the latter are applicable. For more detailed information, see also the PCT Applicant's Guide, a publication of WIPO.

In these Notes, "Article", "Rule", and "Section" refer to the provisions of the PCT, the PCT Regulations and the PCT Administrative Instructions, respectively.

INSTRUCTIONS CONCERNING AMENDMENTS UNDER ARTICLE 19

The applicant has, after having received the international search report, one opportunity to amend the claims of the international application. It should however be emphasized that, since all parts of the international application (claims, description and drawings) may be amended during the international preliminary examination procedure, there is usually no need to file amendments of the claims under Article 19 except where, e.g. the applicant wants the latter to be published for the purposes of provisional protection or has another reason for amending the claims before international publication. Furthermore, it should be emphasized that provisional protection is available in some States only.

What parts of the international application may be amended?

Under Article 19, only the claims may be amended.

During the international phase, the claims may also be amended (or further amended) under Article 34 before the International Preliminary Examining Authority. The description and drawings may only be amended under Article 34 before the International Examining Authority.

Upon entry into the national phase, all parts of the international application may be amended under Article 28 or, where applicable, Article 41.

When?

Within 2 months from the date of transmittal of the international search report or 16 months from the priority date, whichever time limit expires later. It should be noted, however, that the amendments will be considered as having been received on time if they are received by the International Bureau after the expiration of the applicable time limit but before the completion of the technical preparations for international publication (Rule 46.1).

Where not to file the amendments?

The amendments may only be filed with the International Bureau and not with the receiving Office or the International Searching Authority (Rule 46.2).

Where a demand for international preliminary examination has been/is filed, see below.

How?

Either by cancelling one or more entire claims, by adding one or more new claims or by amending the text of one or more of the claims as filed.

A replacement sheet must be submitted for each sheet of the claims which, on account of an amendment or amendments, differs from the sheet originally filed.

All the claims appearing on a replacement sheet must be numbered in Arabic numerals. Where a claim is cancelled, no renumbering of the other claims is required. In all cases where claims are renumbered, they must be renumbered consecutively (Administrative Instructions, Section 205(b)).

The amendments must be made in the language in which the international application is to be published.

What documents must/may accompany the amendments?

Letter (Section 205(b)):

The amendments must be submitted with a letter.

The letter will not be published with the international application and the amended claims. It should not be confused with the "Statement under Article 19(1)" (see below, under "Statement under Article 19(1)").

The letter must be in English or French, at the choice of the applicant. However, if the language of the international application is English, the letter must be in English; if the language of the international application is French, the letter must be in French.

NOTES TO FORM PCT/ISA/220 (continued)

The letter must indicate the differences between the claims as filed and the claims as amended. It must, in particular, indicate, in connection with each claim appearing in the international application (it being understood that identical indications concerning several claims may be grouped), whether

- (i) the claim is unchanged;
- (ii) the claim is cancelled;
- (iii) the claim is new;
- (iv) the claim replaces one or more claims as filed;
- (v) the claim is the result of the division of a claim as filed.

The following examples illustrate the manner in which amendments must be explained in the accompanying letter:

1. [Where originally there were 48 claims and after amendment of some claims there are 51]:
"Claims 1 to 29, 31, 32, 34, 35, 37 to 48 replaced by amended claims bearing the same numbers; claims 30, 33 and 36 unchanged; new claims 49 to 51 added."
2. [Where originally there were 15 claims and after amendment of all claims there are 11]:
"Claims 1 to 15 replaced by amended claims 1 to 11."
3. [Where originally there were 14 claims and the amendments consist in cancelling some claims and in adding new claims]:
"Claims 1 to 6 and 14 unchanged; claims 7 to 13 cancelled; new claims 15, 16 and 17 added." or
"Claims 7 to 13 cancelled; new claims 15, 16 and 17 added; all other claims unchanged."
4. [Where various kinds of amendments are made]:
"Claims 1-10 unchanged; claims 11 to 13, 18 and 19 cancelled; claims 14, 15 and 16 replaced by amended claim 14; claim 17 subdivided into amended claims 15, 16 and 17; new claims 20 and 21 added."

"Statement under article 19(1)" (Rule 46.4)

The amendments may be accompanied by a statement explaining the amendments and indicating any impact that such amendments might have on the description and the drawings (which cannot be amended under Article 19(1)).

The statement will be published with the international application and the amended claims.

It must be in the language in which the international application is to be published.

It must be brief, not exceeding 500 words if in English or if translated into English.

It should not be confused with and does not replace the letter indicating the differences between the claims as filed and as amended. It must be filed on a separate sheet and must be identified as such by a heading, preferably by using the words "Statement under Article 19(1)."

It may not contain any disparaging comments on the international search report or the relevance of citations contained in that report. Reference to citations, relevant to a given claim, contained in the international search report may be made only in connection with an amendment of that claim.

Consequence if a demand for international preliminary examination has already been filed

If, at the time of filing any amendments and any accompanying statement, under Article 19, a demand for international preliminary examination has already been submitted, the applicant must preferably, at the time of filing the amendments (and any statement) with the International Bureau, also file with the International Preliminary Examining Authority a copy of such amendments (and of any statement) and, where required, a translation of such amendments for the procedure before that Authority (see Rules 55.3(a) and 62.2, first sentence). For further information, see the Notes to the demand form (PCT/IPEA/401).

Consequence with regard to translation of the international application for entry into the national phase

The applicant's attention is drawn to the fact that, upon entry into the national phase, a translation of the claims as amended under Article 19 may have to be furnished to the designated/elected Offices, instead of, or in addition to, the translation of the claims as filed.

For further details on the requirements of each designated/elected Office, see Volume II of the PCT Applicant's Guide.

PCT

INTERNATIONAL SEARCH REPORT

(PCT Article 18 and Rules 43 and 44)

Applicant's or agent's file reference 661102	FOR FURTHER ACTION see Notification of Transmittal of International Search Report (Form PCT/ISA/220) as well as, where applicable, item 5 below.	
International application No. PCT/JP 99/ 03929	International filing date (day/month/year) 22/07/1999	(Earliest) Priority Date (day/month/year) 24/07/1998
Applicant SAGAMI CHEMICAL RESEARCH CENTER et al.		

This International Search Report has been prepared by this International Searching Authority and is transmitted to the applicant according to Article 18. A copy is being transmitted to the International Bureau.

This International Search Report consists of a total of 10 sheets.
☐ It is also accompanied by a copy of each prior art document cited in this report.

1. Basis of the report

- a. With regard to the **language**, the international search was carried out on the basis of the international application in the language in which it was filed, unless otherwise indicated under this item.
- ☐ the international search was carried out on the basis of a translation of the international application furnished to this Authority (Rule 23.1(b)).
- b. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international search was carried out on the basis of the sequence listing :
- ☒ contained in the international application in written form.
- ☐ filed together with the international application in computer readable form.
- ☐ furnished subsequently to this Authority in written form.
- ☒ furnished subsequently to this Authority in computer readable form.
- ☒ the statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.
- ☒ the statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished

2. ☐ Certain claims were found unsearchable (See Box I).

3. ☒ Unity of invention is lacking (see Box II).

4. With regard to the **title**,

- ☒ the text is approved as submitted by the applicant.
- ☐ the text has been established by this Authority to read as follows:

5. With regard to the **abstract**,

- ☒ the text is approved as submitted by the applicant.
- ☐ the text has been established, according to Rule 38.2(b), by this Authority as it appears in Box III. The applicant may, within one month from the date of mailing of this international search report, submit comments to this Authority.

6. The figure of the **drawings** to be published with the abstract is Figure No. _____

- ☐ as suggested by the applicant. ☐ None of the figures.
- ☐ because the applicant failed to suggest a figure.
- ☐ because this figure better characterizes the invention.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: Claims 1-6 partially

A protein comprising amino acid sequence SEQ ID NO 1, a DNA SEQ ID NO 11 or 21, encoding this protein, as well as an expression vector capable of expressing this sequence and a eukaryotic cell expressing the DNA

2. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 2 and DNA SEQ ID 12 and 22

3. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 3 and DNA SEQ ID 13 and 23

4. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 4 and DNA SEQ ID 14 and 24

5. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 5 and DNA SEQ ID 15 and 25

6. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 6 and DNA SEQ ID 16 and 36

7. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 7 and DNA SEQ ID 17 and 37

8. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 8 and DNA SEQ ID 18 and 38

9. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 9 and DNA SEQ ID 19 and 39

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

10. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 10 and
DNA SEQ ID 20 and 30

11. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 31 and
DNA SEQ ID 41 and 51

12. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 32 and
DNA SEQ ID 42 and 52

13. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 33 and
DNA SEQ ID 43 and 53

14. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 34 and
DNA SEQ ID 44 and 54

15. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 35 and
DNA SEQ ID 45 and 55

16. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 36 and
DNA SEQ ID 46 and 56

17. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 37 and
DNA SEQ ID 47 and 57

18. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 38 and
DNA SEQ ID 48 and 58

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

19. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 39 and
DNA SEQ ID 49 and 59

20. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 40 and
DNA SEQ ID 50 and 60

21. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 61 and
DNA SEQ ID 71 and 81

22. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 62 and
DNA SEQ ID 72 and 82

23. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 63 and
DNA SEQ ID 73 and 83

24. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 64 and
DNA SEQ ID 74 and 84

25. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 65 and
DNA SEQ ID 75 and 85

26. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 66 and
DNA SEQ ID 76 and 86

27. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 67 and
DNA SEQ ID 77 and 87

28. Claims: 1-6 partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as subject 1 but limited to protein SEQ ID NO. 68 and
DNA SEQ ID 78 and 88

29. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 69 and
DNA SEQ ID 79 and 89

30. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 70 and
DNA SEQ ID 80 and 90

31. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 91 and
DNA SEQ ID 101 and 111

32. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 92 and
DNA SEQ ID 102 and 112

33. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 93 and
DNA SEQ ID 103 and 113

34. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 94 and
DNA SEQ ID 104 and 114

35. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 95 and
DNA SEQ ID 105 and 115

36. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 96 and
DNA SEQ ID 106 and 116

37. Claims: 1-6 partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as subject 1 but limited to protein SEQ ID NO. 97 and
DNA SEQ ID 107 and 117

38. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 98 and
DNA SEQ ID 108 and 118

39. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 99 and
DNA SEQ ID 109 and 119

40. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 100 and
DNA SEQ ID 110 and 120

41. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 121 and
DNA SEQ ID 131 and 141

42. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 122 and
DNA SEQ ID 132 and 142

43. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 123 and
DNA SEQ ID 133 and 143

44. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 124 and
DNA SEQ ID 134 and 144

45. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 125 and
DNA SEQ ID 135 and 145

46. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 126 and

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

DNA SEQ ID 136 and 146

47. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 127 and
DNA SEQ ID 137 and 147

48. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 128 and
DNA SEQ ID 138 and 148

49. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 129 and
DNA SEQ ID 139 and 149

50. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 130 and
DNA SEQ ID 140 and 150

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/JP 99/03929

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/705 C12N5/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 21328 A (KATO SEISHI ;PROTEGENE INC (JP); SEKINE SHINGO (JP); SAGAMI CHEM R) 22 May 1998 (1998-05-22) abstract page 17, last paragraph -page 18, paragraph 1	1-6
X	--- DATABASE EMBLEMEST6 [Online] Accession Number AI057511, 22 July 1998 (1998-07-22) STRAUSBERG R: "H. sapiens cDNA clone IMAGE:1653181 3' similar to SW:YJK4 yeast P42929 hypothetical 16.2 kD protein in SME1-MEF2 intergenic region" XP002123564 100% identity in 357 BP overlap with SEQ ID NO:11 --- -/-	1-6

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

G document member of the same patent family

Date of the actual completion of the international search

23 November 1999

Date of mailing of the international search report

06.03.00

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

CUPIDO, M

INTERNATIONAL SEARCH REPORT

International Application No

PCT/JP 99/03929

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBLEST21 [Online] Accession Number AA 482452, 24 June 1997 (1997-06-24) HILLIER L ET AL.: "zv05b11.r1 Soares NhhMPu S1 Homo sapiens cDNA clone 7527733 5'similar to SW:YJK4 yeast P42929 hypothetical 16.2 kD protein in SME1-MEF2 intergenic region" XP002123565 99.7% identity in 367 BP overlap with SEQ ID NO 11</p>	1-6
A	<p>--- D'ANDREA ET AL: "Molecular Cloning of NKB1. A Natural Killer Cell Receptor for HLA -B Allotypes" JOURNAL OF IMMUNOLOGY, vol. 155, no. 5, 1 September 1995 (1995-09-01), pages 2306-2310 2310, XP002111500 ISSN: 0022-1767 abstract page 2307, right-hand column, line 16</p>	1-6
A	<p>--- GILLEN C M ET AL: "Molecular cloning and functional expression of the K-Cl cotransporter from rabbit, rat, and human." JOURNAL OF BIOLOGICAL CHEMISTRY., vol. 271, no. 27, 5 July 1996 (1996-07-05), pages 16237-16244, XP002119528 AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD., US ISSN: 0021-9258 abstract</p>	1-6
A	<p>--- KYTE J ET AL: "A SIMPLE METHOD FOR DISPLAYING THE HYDROPATHIC CHARACTER OF A PROTEIN" JOURNAL OF MOLECULAR BIOLOGY, vol. 157, no. 1, 5 May 1982 (1982-05-05), pages 105-132, XP000609692 ISSN: 0022-2836 cited in the application the whole document</p>	1-6
P,X	<p>--- DATABSE EMBLEST11 [Online] Accession Number AI 553893, 25 March 1999 (1999-03-25) STRAUSBERG R: "Homo sapiens cDNA clone IMAGE:2169115 3'" XP002123566 100% identity in 375 BP overlap with SEQ ID 11</p> <p>-----</p>	1-6

Effect on patent family members

Personal Application No

PCI/JP 99/03929

Form PCT/ISA/210 (patent family annex) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP 99/03929

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheets

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-6 partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 15/12, C07K 14/705, C12N 5/10		A3	(11) International Publication Number: WO 00/05367 (43) International Publication Date: 3 February 2000 (03.02.00)
(21) International Application Number: PCT/JP99/03929 (22) International Filing Date: 22 July 1999 (22.07.99)			(74) Agents: AOYAMA, Tamotsu et al.; Aoyama & Partners, IMP Building, 3-7, Shiromi 1-chome, Chuo-ku, Osaka-shi, Osaka 540-0001 (JP).
(30) Priority Data: 10/208820 24 July 1998 (24.07.98) JP 10/224105 7 August 1998 (07.08.98) JP 10/238116 25 August 1998 (25.08.98) JP 10/254736 9 September 1998 (09.09.98) JP 10/275505 29 September 1998 (29.09.98) JP			(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
(71) Applicants (for all designated States except US): SAGAMI CHEMICAL RESEARCH CENTER [JP/JP]; 4-1, Nishi-Ohnuma 4-chome, Sagamihara-shi, Kanagawa 229-0012 (JP). PROTEGENE INC. [JP/JP]; 2-20-3, Naka-cho, Meguro-ku, Tokyo 153-0065 (JP). (72) Inventors; and (75) Inventors/Applicants (for US only): KATO, Seishi [JP/JP]; 3-46-50, Wakamatsu, Sagamihara-shi, Kanagawa 229-0014 (JP). KIMURA, Tomoko [JP/JP]; 302, 4-1-28, Nishiikuta, Tama-ku, Kawasaki-shi, Kanagawa 214-0037 (JP).			Published With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments. (88) Date of publication of the international search report: 4 May 2000 (04.05.00)

(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS

(57) Abstract

The present invention provides human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic cells expressing these DNAs.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece			TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	NZ	New Zealand		
CM	Cameroon		Republic of Korea	PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Licchtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

A: D
PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/12, C07K 14/705, C12N 5/10		A2	(11) International Publication Number: WO 00/05367
			(43) International Publication Date: 3 February 2000 (03.02.00)
(21) International Application Number: PCT/JP99/03929 (22) International Filing Date: 22 July 1999 (22.07.99) (30) Priority Data: 10/208820 24 July 1998 (24.07.98) JP 10/224105 7 August 1998 (07.08.98) JP 10/238116 25 August 1998 (25.08.98) JP 10/254736 9 September 1998 (09.09.98) JP 10/275505 29 September 1998 (29.09.98) JP (71) Applicants (for all designated States except US): SAGAMI CHEMICAL RESEARCH CENTER [JP/JP]; 4-1, Nishi-Ohnuma 4-chome, Sagamihara-shi, Kanagawa 229-0012 (JP). PROTEGENE INC. [JP/JP]; 2-20-3, Naka-cho, Meguro-ku, Tokyo 153-0065 (JP). (72) Inventors; and (75) Inventors/Applicants (for US only): KATO, Seishi [JP/JP]; 3-46-50, Wakamatsu, Sagamihara-shi, Kanagawa 229-0014 (JP). KIMURA, Tomoko [JP/JP]; 302, 4-1-28, Nishiikuta, Tama-ku, Kawasaki-shi, Kanagawa 214-0037 (JP).		(74) Agents: AOYAMA, Tamotsu et al.; Aoyama & Partners, IMP Building, 3-7, Shiromi 1-chome, Chuo-ku, Osaka-shi, Osaka 540-0001 (JP). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published Without international search report and to be republished upon receipt of that report.	
(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS			
(57) Abstract			
The present invention provides human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic cells expressing these DNAs.			

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

DESCRIPTION

Human Proteins Having Hydrophobic
Domains and DNAs Encoding These Proteins

5

TECHNICAL FIELD

The present invention relates to human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic cells expressing these DNAs. The proteins of the present invention can be employed as pharmaceuticals or as antigens for preparing antibodies against these proteins. The human cDNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the cDNAs can be utilized as gene sources for large-scale production of the proteins encoded by these cDNAs. Cells into which these genes are introduced to express secretory proteins and membrane proteins in large amounts can be utilized for detection of the corresponding receptors and ligands, screening of novel low-molecular pharmaceuticals, and so on.

20

BACKGROUND ART

Cells secrete many proteins outside the cells. These secretory proteins play important roles for the proliferation control, the differentiation induction, the material transportation, the biological protection, etc. in the cells. Different from intracellular proteins, the secretory proteins exert their actions outside the cells, whereby they can be administered in the intracorporeal manner such as the injection or the drip, so that there are

25

30

hidden potentialities as medicines. In fact, a number of human secretory proteins such as interferons, interleukins, erythropoietin, thrombolytic agents, etc. have been currently employed as medicines. In addition, secretory proteins other than those described above have been undergoing clinical trials to develop as pharmaceuticals. Because it has been conceived that the human cells still produce many unknown secretory proteins, availability of these secretory proteins as well as genes coding for them is expected to lead to development of novel pharmaceuticals utilizing these proteins.

On the other hand, membrane proteins play important roles, as signal receptors, ion channels, transporters, etc. in the material transportation and the information transmission through the cell membrane. Examples thereof include receptors for a variety of cytokines, ion channels for the sodium ion, the potassium ion, the chloride ion, etc., transporters for saccharides and amino acids, and so on, where the genes for many of them have been cloned already. It has been clarified that abnormalities of these membrane proteins are associated with a number of hitherto-cryptogenic diseases. Therefore, discovery of a new membrane protein is anticipated to lead to elucidation of the causes of many diseases, so that isolation of a new gene coding for the membrane protein has been desired.

Heretofore, owing to difficulty in the purification from human cells, these secretory proteins and membrane proteins have been isolated by an approach from the gene side. A general method is the so-called expression cloning which comprises introduction of a cDNA library into eucaryotic cells to express cDNAs and then screening of the cells secreting, or expressing on the surface of membrane,

the objective active protein. However, this method is applicable only to cloning of a gene for a protein with a known function.

5 In general, secretory proteins and membrane proteins possess at least one hydrophobic domain inside the proteins, wherein, after synthesis thereof in the ribosome, this domain works as a secretory signal or remains in the phospholipid membrane to be trapped in the membrane. Accordingly, the evidence of this cDNA for encoding a
10 secretory protein and a membrane protein is provided by determination of the whole base sequence of a full-length cDNA followed by detection of highly hydrophobic domain(s) in the amino acid sequence of the protein encoded by this cDNA.

15

OBJECTS OF THE INVENTION

The main object of the present invention is to provide novel human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as
20 well as transformed eucaryotic cells that are capable of expressing these DNAs. This object as well as other objects and advantages of the present invention will become apparent to those skilled in the art from the following description with reference to the accompanying drawings.

25

BRIEF DESCRIPTION OF DRAWINGS

Fig. 1 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01550.

Fig. 2 illustrates the hydrophobicity/hydrophilicity
30 profile of the protein encoded by clone HP02593.

Fig. 3 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10195.

Fig. 4 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10423.

Fig. 5 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10506.

5 Fig. 6 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10507.

Fig. 7 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10548.

10 Fig. 8 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10566.

Fig. 9 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10567.

Fig. 10 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10568.

15 Fig. 11 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01426.

Fig. 12 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02515.

20 Fig. 13 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02575.

Fig. 14 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10357.

Fig. 15 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10447.

25 Fig. 16 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10477.

Fig. 17 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10513.

30 Fig. 18 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10540.

Fig. 19 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10557.

Fig. 20 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10563.

Fig. 21 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01467.

5 Fig. 22 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01956.

Fig. 23 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02545.

10 Fig. 24 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02551.

Fig. 25 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02631.

Fig. 26 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02632.

15 Fig. 27 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10488.

Fig. 28 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10538.

20 Fig. 29 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10542.

Fig. 30 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10571.

Fig. 31 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01470.

25 Fig. 32 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02419.

Fig. 33 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02631.

30 Fig. 34 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02695.

Fig. 35 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10031.

Fig. 36 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10530.

Fig. 37 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10541.

5 Fig. 38 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10550.

Fig. 39 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10590.

10 Fig. 40 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10591.

Fig. 41 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01462.

Fig. 42 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02485.

15 Fig. 43 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02798.

Fig. 44 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10041.

20 Fig. 45 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10246.

Fig. 46 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10392.

Fig. 47 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10489.

25 Fig. 48 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10519.

Fig. 49 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10531.

30 Fig. 50 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10574.

SUMMARY OF THE INVENTION

As the result of intensive studies, the present inventors have been successful in cloning of cDNAs coding for proteins having hydrophobic domains from the human full-length cDNA bank, thereby completing the present invention.

5 In other words, the present invention provides human proteins having hydrophobic domains, namely proteins comprising any of the amino acid sequences represented by SEQ ID Nos. 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130. Moreover, the present invention provides DNAs coding

10 for the above-mentioned proteins, exemplified by cDNAs comprising any of the base sequences represented by SEQ ID Nos. 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140, as well as expression vectors that are capable of expressing any of these DNAs by in vitro translation or in

15 eucaryotic cells and transformed eucaryotic cells that are capable of expressing these DNAs and of producing the above-mentioned proteins.

DETAILED DESCRIPTION OF THE INVENTION

20 The proteins of the present invention can be obtained, for example, by a method for isolation from human organs, cell lines, etc., a method for preparation of peptides by the chemical synthesis, or a method for production with the recombinant DNA technology using the DNAs coding for the

25 hydrophobic domains of the present invention, among which the method for production with the recombinant DNA technology is employed preferably. For instance, in vitro expression of the proteins can be achieved by preparation of an RNA by in vitro transcription from a vector having one of

30 the cDNAs of the present invention, followed by in vitro translation using this RNA as a template. Also, introduction of the translated region into a suitable expression vector

by the method known in the art leads to expression of a large amount of the encoded protein in prokaryotic cells such as *Escherichia coli*, *Bacillus subtilis*, etc., and eucaryotic cells such as yeasts, insect cells, mammalian cells, etc.

In the case where one of the proteins of the present invention is produced by expressing the DNA by in vitro translation, the protein of the present invention can be produced in vitro, when the translated region of this cDNA is introduced into a vector having an RNA polymerase promoter, followed by addition of the vector to an in vitro translation system such as a rabbit reticulocyte lysate or a wheat germ extract, containing an RNA polymerase corresponding to the promoter. RNA polymerase promoters are exemplified by T7, T3, SP6, and the like. The vectors containing these RNA polymerase promoters are exemplified by pKA1, pCDM8, pT3/T7 18, pT7/3 19, pBluescript II, and so on. Furthermore, the protein of the present invention can be expressed as the secreted form or the form incorporated into the microsome membrane, when a canine pancreas microsome or the like is added to the reaction system.

In the case where one of the protein of the present invention is produced by expressing the DNA in a microorganism such as *Escherichia coli* etc., a recombinant expression vector bearing the translated region of the cDNA of the present invention is constructed in an expression vector having an origin which can be replicated in the microorganism, a promoter, a ribosome-binding site, a cDNA-cloning site, a terminator etc. and, after transformation of the host cells with this expression vector, the resulting transformant is incubated, whereby the protein encoded by said cDNA can be produced on a large scale in the

microorganism. In this case, a protein fragment containing any region can be obtained by carrying out the expression with inserting an initiation codon and a termination codon in front of and behind the selected translated region.

5 Alternatively, a fusion protein with another protein can be expressed. Only the portion of the protein encoded by this cDNA can be obtained by cleavage of this fusion protein with a suitable protease. The expression vector for *Escherichia coli* is exemplified by the pUC series, pBluescript II, the

10 pET expression system, the pGEX expression system, and so on.

In the case where one of the proteins of the present invention is produced by expressing the DNA in eucaryotic cells, the protein of the present invention can be produced as a secretory protein or as a membrane protein on the cell-

15 membrane surface, when the translated region of this cDNA is introduced into an expression vector for eucaryotic cells that has a promoter, a splicing region, a poly(A) addition site, etc., followed by introduction into the eucaryotic cells. The expression vector is exemplified by pKA1,

20 pED6dpc2, pCDM8, pSVK3, pMSG, pSVL, pBK-CMV, pBK-RSV, EBV vector, pRS, pYES2, and so on. Examples of eucaryotic cells to be used in general include mammalian cultured cells such as simian kidney cells COS7, Chinese hamster ovary cells CHO, etc., budding yeasts, fission yeasts, silkworm cells,

25 *Xenopus* oocytes, and so on, but any eucaryotic cells may be used, provided that they are capable of expressing the proteins of the present invention. The expression vector can be introduced into the eucaryotic cells by methods known in the art such as the electroporation method, the calcium

30 phosphate method, the liposome method, the DEAE-dextran method, and so on.

After one of the proteins of the present invention is

expressed in prokaryotic cells or eucaryotic cells, the objective protein can be isolated from the culture and purified by a combination of separation procedures known in the art. Such examples include treatment with a denaturing agent such as urea or a detergent, sonication, enzymatic digestion, salting-out or solvent precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric focusing, ion-exchange chromatography, hydrophobic chromatography, affinity chromatography, reverse phase chromatography, and so on.

The proteins of the present invention include peptide fragments (5 amino acid residues or more) containing any partial amino acid sequence in the amino acid sequences represented by SEQ ID Nos. 1. to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130. These peptide fragments can be utilized as antigens for preparation of antibodies. Hereupon, among the proteins of the present invention, those having the signal sequences are secreted in the form of mature proteins, after the signal sequences are removed. Therefore, these mature proteins shall come within the scope of the present invention. The N-terminal amino acid sequences of the mature proteins can be easily determined by using the method for the determination of cleavage site of a signal sequence [JP 8-187100 A]. Furthermore, some membrane proteins undergo the processing on the cell surface to be converted to the secretory forms. Such proteins or peptides in the secretory forms shall come within the scope of the present invention. In the case where sugar chain-binding sites are present in the amino acid sequences, expression in appropriate eucaryotic cells affords proteins to which sugar chains are attached. Accordingly, such proteins or peptides to which sugar chains are attached shall come within the

scope of the present invention.

The DNAs of the present invention include all the DNAs coding for the above-mentioned proteins. These DNAs can be obtained by using a method by chemical synthesis, a method
5 by cDNA cloning, and so on.

The cDNAs of the present invention can be cloned, for example, from cDNA libraries derived from the human cells. These cDNAs are synthesized by using as templates poly(A)⁺ RNAs extracted from human cells. The human cells may be
10 cells delivered from the human body, for example, by the operation or may be the cultured cells. The cDNAs can be synthesized by using any method selected from the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and
15 Hoffman, J. Gene 25: 263-269 (1983)], and so on, but it is preferred to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)], as exemplified in Examples, in order to obtain a full-length clone in an effective manner. In addition, commercially available, human cDNA libraries can
20 be utilized. Cloning of the cDNAs of the present invention from the cDNA libraries can be carried out by synthesis of an oligonucleotide on the basis of base sequences of any portion in the cDNA of the present invention, followed by screening using this oligonucleotide as the probe according
25 to the colony or plaque hybridization by a method known in the art. In addition, the cDNA fragments of the present invention can be prepared by synthesis of oligonucleotides which hybridize with both termini of the objective cDNA fragment, followed by the usage of these oligonucleotides as
30 the primers for the RT-PCR method using an mRNA isolated from human cells.

The cDNAs of the present invention are characterized by

comprising either of the base sequences represented by SEQ ID Nos. 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140 or the base sequences represented by SEQ ID Nos. 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150. Table 1
5 summarizes the clone number (HP number), the cells from which the cDNA was obtained, the total base number of the cDNA, and the number of the amino acid residues of the encoded protein, for each of the cDNAs.

Table 1

SEQ ID No.	HP number	Cells	Base number	Number of amino acid residues
1, 11, 21	HP01550	Stomach cancer	510	125
2, 12, 22	HP02593	Saos-2	697	131
3, 13, 23	HP10195	HT-1080	1619	242
4, 14, 24	HP10423	U-2 OS	1066	264
5, 15, 25	HP10506	Stomach cancer	618	112
6, 16, 26	HP10507	Stomach cancer	1021	146
7, 17, 27	HP10548	Stomach cancer	1432	344
8, 18, 28	HP10566	Stomach cancer	601	97
9, 19, 29	HP10567	Stomach cancer	585	124
10, 20, 30	HP10568	Stomach cancer	1100	327
31, 41, 51	HP01426	Stomach cancer	1065	313
32, 42, 52	HP02515	Saos-2	937	229
33, 43, 53	HP02575	Saos-2	1678	467
34, 44, 54	HP10357	Stomach cancer	467	99
35, 45, 55	HP10447	Liver	875	189
36, 46, 56	HP10477	Liver	1256	363
37, 47, 57	HP10513	Stomach cancer	884	249
38, 48, 58	HP10540	Saos-2	589	98
39, 49, 59	HP10557	Stomach cancer	673	172
40, 50, 60	HP10563	Saos-2	1425	120
61, 71, 81	HP01467	HT-1080	1436	307
62, 72, 82	HP01956	Liver	997	183
63, 73, 83	HP02545	Saos-2	1753	327
64, 74, 84	HP02551	Saos-2	1117	223
65, 75, 85	HP02631	Saos-2	1380	48
66, 76, 86	HP02632	HT-1080	1503	371
67, 77, 87	HP10488	Liver	733	90
68, 78, 88	HP10538	Saos-2	3768	499
69, 79, 89	HP10542	Stomach cancer	770	106
70, 80, 90	HP10571	Stomach cancer	1229	152

91, 101, 111	HP01470	Stomach cancer	1619	358
92, 102, 112	HP02419	Stomach cancer	2054	226
93, 103, 113	HP02631	Saos-2	1380	195
94, 104, 114	HP02695	Stomach cancer	1292	339
95, 105, 115	HP10031	Saos-2	2168	487
96, 106, 116	HP10530	Saos-2	1357	393
97, 107, 117	HP10541	Stomach cancer	711	196
98, 108, 118	HP10550	Stomach cancer	651	107
99, 109, 119	HP10590	HT-1080	1310	350
100, 110, 120	HP10591	HT-1080	1400	107
121, 131, 141	HP01462	HT-1080	2050	483
122, 132, 142	HP02485	Stomach cancer	2746	334
123, 133, 143	HP02798	HT-1080	1136	267
124, 134, 144	HP10041	Saos-2	619	106
125, 135, 145	HP10246	KB	864	224
126, 136, 146	HP10392	U-2 OS	1527	258
127, 137, 147	HP10489	Stomach cancer	659	110
128, 138, 148	HP10519	Stomach cancer	710	91
129, 139, 149	HP10531	Saos-2	2182	344
130, 140, 150	HP10574	Stomach cancer	2773	428

Hereupon, the same clones as the cDNAs of the present invention can be easily obtained by screening of the cDNA libraries constructed from the human cell lines or human tissues utilized in the present invention by the use of an oligonucleotide probe synthesized on the basis of the cDNA base sequence described in any of SEQ ID Nos. 11 to 30, 41 to 60, 71 to 90, 101 to 120, and 131 to 150.

In general, the polymorphism due to the individual difference is frequently observed in human genes. Accordingly, any cDNA in which one or plural nucleotides are inserted, deleted and/or substituted with other nucleotides in SEQ ID Nos. 11 to 30, 41 to 60, 71 to 90, 101 to 120, and

131 to 150 shall come within the scope of the present invention.

In a similar manner, any protein in which one or plural amino acids are inserted, deleted and/or substituted with other amino acids shall come within the scope of the present invention, as far as the protein possesses the activity of any protein having the amino acid sequences represented by SEQ ID Nos. 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130.

The cDNAs of the present invention include cDNA fragments (10 bp or more) containing any partial base sequence in the base sequences represented by SEQ ID Nos. 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140 or in the base sequences represented by SEQ ID Nos. 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150. Also, DNA fragments consisting of a sense strand and an anti-sense strand shall come within this scope. These DNA fragments can be utilized as the probes for the genetic diagnosis.

In addition to the activities and uses described above, the polynucleotides and proteins of the present invention may exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant

protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine

levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be

administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular

Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of
5 spleen cells, lymph node cells or thymocytes include,
without limitation, those described in: Polyclonal T cell
stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current
Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp.
3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and
10 Measurement of mouse and human Interferon γ , Schreiber, R.D.
In Current Protocols in Immunology. J.E.e.a. Coligan eds.
Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of
hematopoietic and lymphopoietic cells include, without
15 limitation, those described in: Measurement of Human and
Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis,
L.S. and Lipsky, P.E. In Current Protocols in Immunology.
J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and
Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-
20 1211, 1991; Moreau et al., Nature 336:690-692, 1988;
Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-
2938, 1983; Measurement of mouse and human interleukin 6-
Nordan, R. In Current Protocols in Immunology. J.E.e.a.
Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons,
25 Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A.
83:1857-1861, 1986; Measurement of human Interleukin 11 -
Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J.
In Current Protocols in Immunology. J.E.e.a. Coligan eds.
Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991;
30 Measurement of mouse and human Interleukin 9 - Ciarletta, A.,
Giannotti, J., Clark, S.C. and Turner, K.J. In Current
Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp.

6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp.

and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

5 Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune
10 thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly
15 allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

 Using the proteins of the invention it may also be
20 possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by
25 suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing
30 non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent

has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen
5 functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD).
10 For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the
15 transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an
20 activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen
25 function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by
30 B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or

tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating

autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the commoncold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the

transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

5 In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can
10 be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the
15 expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell.
20 Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary
25 costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected
30 with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β microglobulin protein or an MHC class

II chain protein and an MHC class II chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J.

Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

5 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J.J. and Brunswick, M. In
10 Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly
15 Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse
20 Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that
25 activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine
30 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965,

1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

5 Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808,
10 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology
15 1:639-648, 1992.

 Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et
20 al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

 A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the
25 treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells
30 alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to

stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and

Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is

not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

10 A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

20 Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or
5 ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells,
10 induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel
15 syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of
20 nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the
25 treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager
30 syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head

trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

5 Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

10 It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including
15 vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

20 A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

25 A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

30 Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon);

International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without
5 limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

10 A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of
15 follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals.
20 Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- group, may be useful as a fertility inducing therapeutic, based upon the
25 ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime
30 reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among

other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; 5 Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic 10 or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a 15 desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or 20 neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or 25 indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing 30 such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among

other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include,

without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22),

Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al.,
5 Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in
10 the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production
15 of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)),
20 ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the
25 invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for
30 immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A

protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues
5 necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth

10 Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria,
15 viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast
20 augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid,
25 protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and
30 violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of

embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Examples

The present invention is specifically illustrated in more detail by the following Examples, but Examples are not intended to restrict the present invention. The basic operations with regard to the recombinant DNA and the enzymatic reactions were carried out according to the literature ["Molecular Cloning. A Laboratory Manual", Cold Spring Harbor Laboratory, 1989]. Unless otherwise stated, restrictive enzymes and a variety of modification enzymes to be used were those available from Takara Shuzo. The buffer compositions and the reaction conditions for each of the enzyme reactions were as described in the manufacturer's instructions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

(1) Selection of cDNAs Encoding Proteins Having Hydrophobic Domains

The cDNA library of fibrosarcoma cell line HT-1080 (WO98/11217), the cDNA library of osteosarcoma cell line Saos-2 (WO97/33993), the cDNA library of osteosarcoma cell line U-2 OS (WO98/21328), the cDNA library of epidermoid

carcinoma cell line KB (WO98/11217), the cDNA library of tissues of stomach cancer delivered by the operation (WO98/21328), the cDNA library of liver tissue delivered by the operation (WO98/21328), and were used for the cDNA
5 libraries. Full-length cDNA clones were selected from respective libraries and the whole base sequences thereof were determined to construct a homo-protein cDNA bank consisting of the full-length cDNA clones. The hydrophobicity/hydrophilicity profiles were determined for
10 the proteins encoded by the full-length cDNA clones registered in the homo-protein cDNA bank by the Kyte-Doolittle method [Kyte, J. & Doolittle, R. F., J. Mol. Biol. 157: 105-132 (1982)] to examine the presence or absence of a hydrophobic region. Any clone that has a hydrophobic region
15 being putative as a secretory signal or a transmembrane domain in the amino acid sequence of the encoded protein was selected as a clone candidate.

(2) Protein Synthesis by In Vitro Translation

The plasmid vector bearing the cDNA of the present
20 invention was used for in vitro transcription/translation with a T₇T rabbit reticulocyte lysate kit (Promega). In this case, [³⁵S]methionine was added to label the expression product with a radioisotope. Each of the reactions was carried out according to the protocols attached to the kit.
25 Two micrograms of the plasmid was subjected to the reaction at 30°C for 90 minutes in the reaction solution of a total volume of 25 μ l containing 12.5 μ l μ of T₇T rabbit reticulocyte lysate, 0.5 μ l of a buffer solution (attached to the kit), 2 μ l of an amino acid mixture (without
30 methionine), 2 μ l of [³⁵S]methionine (Amersham) (0.37 MBq/ μ l), 0.5 μ l of T7 RNA polymerase, and 20 U of RNasin. Also, an experiment in the presence of a membrane system was carried

out by adding to this reaction system 2.5 μ l of a canine pancreas microsome fraction (Promega). To 3 μ l of the resulting reaction solution was added 2 μ l of the SDS sampling buffer (125 mM Tris-hydrochloric acid buffer, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0.025% bromophenol blue, and 20% glycerol) and the resulting mixture was heated at 95°C for 3 minutes and then subjected to SDS-polyacrylamide gel electrophoresis. The molecular weight of the translation product was determined by carrying out the autoradiography.

(3) Expression by COS7

Escherichia coli cells bearing the expression vector for the protein of the present invention was incubated at 37°C for 2 hours in 2 ml of the 2xYT culture medium containing 100 μ g/ml of ampicillin, the helper phage M13KO7 (50 μ l) was added, and the incubation was continued at 37°C overnight. A supernatant separated by centrifugation underwent precipitation with polyethylene glycol to obtain single-stranded phage particles. These particles were suspended in 100 μ l of 1 mM Tris-0.1 mM EDTA, pH 8 (TE).

The cultured cells derived from simian kidney, COS7, were incubated at 37°C in the presence of 5% CO₂ in the Dulbecco's modified Eagle's culture medium (DMEM) containing 10% fetal calf serum. Into a 6-well plate (Nunc, well diameter: 3 cm) were inoculated with 1×10^5 COS7 cells and incubation was carried out at 37°C for 22 hours in the presence of 5% CO₂. After the culture medium was removed, the cell surface was washed with a phosphate buffer solution and then washed again with DMEM containing 50 mM Tris-hydrochloric acid (pH 7.5) (TDMEM). To the resulting cells was added a suspension of 1 μ l of the single-stranded phage suspension, 0.6 ml of the DMEM culture medium, and 3 μ l of

TRANSFECTAM™ (IBF) and the resulting mixture was incubated at 37°C for 3 hours in the presence of 5% CO₂. After the sample solution was removed, the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf serum was added, and the incubation was carried out at 37°C for 2 days in the presence of 5% CO₂. After the culture medium was replaced by a culture medium containing [³⁵S]cystine or [³⁵S]methionine, the incubation was carried out for one hour. After the culture medium and the cells were separated by centrifugation, proteins in the culture medium fraction and the cell-membrane fraction were subjected to SDS-PAGE.

(4) Clone Examples

<HP01550> (SEQ ID Nos. 1, 11, and 21)

Determination of the whole base sequence of the cDNA insert of clone HP01550 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 65-bp 5'-untranslated region, a 378-bp ORF, and a 67-bp 3'-untranslated region. The ORF codes for a protein consisting of 125 amino acid residues and there existed one putative transmembrane domain. Figure 1 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 15 kDa that was almost identical with the molecular weight of 13,825 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein F45G2.c (GenBank Accession No. Z93382). Table 2 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the C.

elegans hypothetical protein F45G2.c (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 44.5% in the entire region.

Table 2

```

10  HP MAKYLAQIIIVMGVQVVGRAFAALRQEF-----AASRAAADARGRAGHRSAASNL-
      . . . . . * . * . * . * . * . * . * . * . * . * . * . * .
CE MPWRTALKVALAAGEAVAKALTRAVRDEIKQTQQAAARHAASGTQSASETRENANSNAKL
HP GLSLQEAQQIILNV-SKLSPEEVQKNYEHLEFKVNDKSVGGSFYLQSKVVRAKERLDEEL-K
      * . * . * . * . * . * . * . * . * . * . * . * . * . * . * .
15  CE GISLEESLQIILNVKTPLNREEVEKHYEHLFNINDKSKGGTLYLQSKVFRAKERIDEEFGR
HP IQAQEDREKGQMPHT
      * . * . * . * . * . *
CE IELKEEKKKEENAKTE

```

20

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA338859) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02593> (SEQ ID Nos. 2, 12, and 22)

30 Determination of the whole base sequence of the cDNA
insert of clone HP02593 obtained from cDNA library of human
osteosarcoma cell line Saos-2 revealed the structure
consisting of a 103-bp 5'-untranslated region, a 396-bp ORF,

5

10

15

20

Table 3

25

OB MAGVKALVALSFSGAIGLTFMLGCALEDYGVYWPLFVLIFHAISPIPHFIAKRVTYDSD

* * * * *

HP GSNDDFSQQW

30

OB GRGDDFSWEOW

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA306490) in ESTs, but, since they
5 are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10195> (SEQ ID Nos. 3, 13, and 23)

10 Determination of the whole base sequence of the cDNA insert of clone HP10195 obtained from cDNA library of human fibrosarcoma HT-1080 revealed the structure consisting of a 286-bp 5'-untranslated region, a 729-bp ORF, and a 604-bp 3'-untranslated region. The ORF codes for a protein
15 consisting of 242 amino acid residues and there existed one putative transmembrane domain at the C-terminus. Figure 3 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation
20 product of 32 kDa that was somewhat larger than the molecular weight of 27,300 predicted from the ORF. When expressed in COS7 cells, an expression product of about 21 kDa was observed in the supernatant fraction and the membrane fraction.

25 The search of the protein data base using the amino acid sequence of the present protein has revealed the registration of sequences that were similar to the Aplysia VAP-33 (SWISS-PROT Accession No. P53173). Table 4 shows the comparison between amino acid sequences of the human protein
30 of the present invention (HP) and the Aplysia VAP-33 (AP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the

present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 46.5% in the entire region.

5

Table 4

	HP	MAKHEQILVLDPPTDLKFKGPFTDVVTNLKLRNPSDRKVCFKVKTAPRRYCVRPNSGI
		.* *.**.*...*.*****.****.***.*****.*****
10	AP	MASHEQALILEPAGELRFKGPFTDVVTADLKLSNPTDRRICFKVKTAPKRYCVRPNSGI
	HP	IDPGSTVTVSVMLQPFYDPNEKSKHKFMVQTIAPPNTSD-MEAVWKEAKPDELMDSKL
		..******.*****.*****..** .. . * .***. *.....**
	AP	LEPKTSIAVAVMLQPFNYDPNEKNKHKFMVQSMYAPDHVVESQELLWKDAPPESLMDTKL
	HP	RCVFEMPENNDKLNDMEPSK-----AVPLNASKQDGPMPKP-HSVSLNDTE
15		*****..... . ..** ... **. *.
	AP	RCVFEMPDGSHQAPASDASRATDAGAHFSESALEDPTVASRKTETQSPKRVGAVGSAGED
	HP	TRKLMEECKRLQGEMMKLSEENRHLRDEGLRLRKVAHSD--KPGSTSTASFRDNVTSLP
		..** . * *. *. * . * . * . * . * . * . * . * . * . * . * . * . * . *
	AP	VKKLQHELKKAQSEITSLKGENSQLKDEGIRLRKVAMTDTVSPTPLNPSPAPAAAVRAFP
20	HP	SLLVVIAAIFIGFFLGKFIL
		... * . * . * . * . * . * . * . *
	AP	PVVYVVAAILGLIIGKFL

25 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA447905) in ESTs, but, since they are partial sequences, it can not be judged whether or not

30 any of these sequences codes for the same protein as the protein of the present invention.

<HP10423> (SEQ ID Nos. 4, 14, and 24)

Determination of the whole base sequence of the cDNA insert of clone HP10423 obtained from cDNA library of human osteosarcoma cell line U-2 OS revealed the structure consisting of a 64-bp 5'-untranslated region, a 795-bp ORF, and a 207-bp 3'-untranslated region. The ORF codes for a protein consisting of 264 amino acid residues and there existed a secretory signal at the N-terminus and one putative transmembrane domain at the N-terminus. Figure 4 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was almost identical with the molecular weight of 29,377 predicted from the ORF. When expressed in COS7 cells, an expression product of about 31 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. D80116) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10506> (SEQ ID Nos. 5, 15, and 25)

Determination of the whole base sequence of the cDNA insert of clone HP10506 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 53-bp 5'-untranslated region, a 339-bp ORF, and a 226-bp 3'-untranslated region. The ORF codes for a protein consisting of 112 amino acid residues and there existed one putative transmembrane domain. Figure 5 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,821 predicted from the ORF. When expressed in
5 COS7 cells, an expression product of about 13 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for
10 example, Accession No. AA282544) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

15 <HP10507> (SEQ ID Nos. 6, 16, and 26)

Determination of the whole base sequence of the cDNA insert of clone HP10507 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 412-bp 5'-untranslated region, a 441-bp ORF, and a 168-bp 3'-
20 untranslated region. The ORF codes for a protein consisting of 146 amino acid residues and there existed a secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 6 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-
25 Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 19 kDa that was somewhat larger than the molecular weight of 16,347 predicted from the ORF.

Furthermore, the search of the GenBank using the base
30 sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA424759) in ESTs, but, since they

are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

5 <HP10548> (SEQ ID Nos. 7, 17, and 27)

Determination of the whole base sequence of the cDNA insert of clone HP10548 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 330-bp 5'-untranslated region, a 1035-bp ORF, and a 67-bp 3'-
10 untranslated region. The ORF codes for a protein consisting of 344 amino acid residues and there existed four putative transmembrane domains. Figure 7 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro
15 translation resulted in formation of a translation product of a high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for
20 example, Accession No. AA143152) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

25 <HP10566> (SEQ ID Nos. 8, 18, and 28)

Determination of the whole base sequence of the cDNA insert of clone HP10566 obtained from cDNA library of the human stomach cancer revealed the structure consisting of a 61-bp 5'-untranslated region, a 294-bp ORF, and a 246-bp 3'-
30 untranslated region. The ORF codes for a protein consisting of 97 amino acid residues and there existed one putative transmembrane domain at the C-terminus. Figure 8 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,452 predicted from the ORF. When expressed in COS7 cells, an expression product of about 12 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W79821) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

15

<HP10567> (SEQ ID Nos. 9, 19, and 29)

Determination of the whole base sequence of the cDNA insert of clone HP10567 obtained from cDNA library of the human stomach cancer revealed the structure consisting of a 77-bp 5'-untranslated region, a 375-bp ORF, and a 133-bp 3'-untranslated region. The ORF codes for a protein consisting of 124 amino acid residues and there existed one putative transmembrane domain at the C-terminus. Figure 9 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 14 kDa that was almost identical with the molecular weight of 14,484 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA428475) in ESTs, but, since they

are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

5 <HP10568> (SEQ ID Nos. 10, 20, and 30)

Determination of the whole base sequence of the cDNA insert of clone HP10568 obtained from cDNA library of the human stomach cancer revealed the structure consisting of a 56-bp 5'-untranslated region, a 984-bp ORF, and a 60-bp 3'-untranslated region. The ORF codes for a protein consisting of 327 amino acid residues and there existed a secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 10 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36.5 kDa that was almost identical with the molecular weight of 34,326 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 40 kDa which is considered to have a sugar chain being attached. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Leu-Thr at position 138 and Asn-Leu-Ser at position 206). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from valine at position 24. When expressed in COS7 cells, an expression product of about 31 kDa was observed in the supernatant fraction and the membrane fraction.

30 The search of the protein data base using the amino acid sequence of the present protein has revealed that the protein was similar to the human cell-surface A33 antigen

(SWISS-PROT Accession No. Q99795). Table 5 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human cell-surface A33 antigen (A3). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 30.0% in the N-terminal region of 243 residues.

Table 5

	HP	MAELPGPFLCGALLGFLCLSGLADEVKVPTEPLSTPLGKTAELTCTYSTSVGDSFAL-EW	
		* . *... **...*..** *..*.. .*
15	A3	MVGKMWPVLWTLCAVRVTVDALSVETPQDVLRASQGKSVTLPCITYHTSTSSREGLIQW	
	HP	SFVQPGKPISESHPILYFTNGHLYPTGSKSKRVSLNQNPPTVGVATLKLTDVHPSDTGTY	
	 *	*..* . * * . * . . * .. * ..*..*..* .*
	A3	DKLL--LTHTERVVIWPFSSNKN-YIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTY	
	HP	LCQVNNPPDFYTNGLGILNLTVLVPPSNPLCSQSGQTSVGGSTALRCSSSEGAPKPVYNW	
20		* * . . * *	*****. * * . * . * ..*..* * *..*..* * *
	A3	ECSVSLMSDLEGNTKSRVRLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPOYSW	
	HP	VRLGTFPTSPGSMVQDEVSGQLILTNLSLTSSGTYRCVATNQMGASCELTLSVTEPS-	
		* *	..* . . . *..* * ..*..* * ..*..*..* .*
	A3	KRYNILNQEQP--LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSM	
25	HP	-QGRVAGALIGVLLGVLLLSVAAFCLVRFQKERGKKPKETYGGSDLREDAIAPGISEHTC	
		. . * . * *	
	A3	NVALYVGIAGVVAALIIIGIIIIYCCCCRGKDDNTEDKEDARPNREAYEEPPEQLRELSR	
	HP	MRADSSKGFLERPSSASTVTTTTSKSLPMVV	
30	A3	EREEEDDYRQEEQIRSTGRES PDHLDQ	

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration

of sequences that shared a homology of 90% or more (for example, Accession No. T24595) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP01426> (SEQ ID Nos. 31, 41, and 51)

Determination of the whole base sequence of the cDNA insert of clone HP01426 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 1-bp 5'-untranslated region, a 942-bp ORF, and a 122-bp 3'-untranslated region. The ORF codes for a protein consisting of 313 amino acid residues and there existed a putative secretory signal. Figure 11 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36 kDa that was almost identical with the molecular weight of 34,955 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 38 kDa which is considered to have a sugar chain being attached after secretion. In addition, there exists in the amino acid sequence of this protein one site at which N-glycosylation may occur (Asn-Ser-Ser at position 163). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from tryptophan at position 17. When expressed in COS7 cells, an expression product of about 39 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the

protein was similar to the *Xenopus laevis* cortical granule lectin (EMBL Accession No. X82626). Table 6 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *X. laevis* cortical granule lectin (XL). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 67.9% in the region other than the N-terminal region.

Table 6

```

15 HP MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRCKEIKDECPSAFDGLYFLRT
    *      **                               *      *****. . * **.* * .
XL MLVHILLLLLVTGGLSQSCEPVVIVASKNMVKQLDCDKFRSCKEIKDSNEEAQDGIYTLTS
HP ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY
    .*. *****. .*****.* *****.*****.*****
20 XL SDGISYQTFCDMTTNGGGWTLVASVHENNMAGKCTIGDRWSSQQGNRADYPEGDGNWANY
HP NTFGSAEAATSDDYKNPGYYDIAQKDLGIWHVPNKSPMQHWRNSSLRYRTDTGFLQTLG
    *****.*****.* .**.******.*. ***** ***.**.* *
XL NTFGSAGGATSDDYKNPGYYDIEAYNLGVWHVPNKTPLSVWRNSSLQRYRTTDGILFKHG
HP HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRV
    ***.**. ***** *.* .*.***.***.*.*. ***.*** ...**.*.***
25 XL GNLFSLYRIYPVKYGIGSCSKDSGPTVPVVYDLGSAKLTASFYSPDFRSQFTPGYIQFRP
HP FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSS
    .*.*** ***.***....**.* *****.*.*****.*.*****. **
XL INTEKAALALCPGMKMESCNVEHVCIGGGGYFPEADPRQCGDFAAYDFNGYGTKKFNSAG
HP REITEAAVLLFYR
30 *****
XL IEITEAAVLLFYL

```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R06009) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02515> (SEQ ID Nos. 32, 42, and 52)

Determination of the whole base sequence of the cDNA insert of clone HP02515 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 176-bp 5'-untranslated region, a 690-bp ORF, and a 71-bp 3'-untranslated region. The ORF codes for a protein consisting of 229 amino acid residues and there existed a putative secretory signal at N-terminus and one putative transmembrane domain at the C-terminus. Figure 12 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was almost identical with the molecular weight of 26,000 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 25.5 kDa from which the secretory signal is considered to have been cleaved. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from phenylalanine at position 28.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human T1/ST2 receptor binding protein (GenBank Accession No. U41804). Table 7 shows the

comparison between amino acid sequences of the human protein of the present invention (HP) and the human T1/ST2 receptor binding protein (T1). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 55.8% in the entire region.

Table 7

```

HP  MGDKIWLFPFVLLLAALPPVLLPGAAGFTPSLSDSFTFTLPAGQKECFYQPMPLKASLE
      *.... ** .*** . *** . * ..*** ***.*****. * .****
T1  MMAAGAALALALWLL--MPPVEV-GGAGPPPIQDGEFTFLLPAGRKQCFYQSAPANASLE
15  HP  IEYQVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVE-TEVGDMFCFDNTFSTISEK
      .*****.*****.** *.***. * ** * **..***** **..***.*****.*****
T1  TEYQVIGGAGLDVDFTLESPQGVLLVSESRKADGVHTVEPTTEAGDYKLCFDNSFSTISEK
HP  VIFFELILDNMGEQAQEEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLR
      ..*****.*.. ....* *. * . . .*****.* **..*.....*..* .. .***
20  T1  LVFFELIFDSL-QDDEEVEGWAEAVEPEEMLDVKMEDIKESIETMRTRLERSIQMLTLRL
HP  AFEARDRNIQESNFDNRVNFWSMVNLVVMVVSAIQVYMLKSLFEDKRKSRT
      *****.*..*..***** **..*.....*..* ..*.....*..* .*
T1  AFEARDRNLQEGNLERNVNFWSAVNVAVLLLVAVLQVCTLKRFFQDKRPVPT

```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA381943) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02575> (SEQ ID Nos. 33, 43, and 53)

Determination of the whole base sequence of the cDNA insert of clone HP02575 obtained from cDNA library of human osteosarcome cell line Saos-2 revealed the structure consisting of a 55-bp 5'-untranslated region, a 1404-bp ORF, and a 219-bp 3'-untranslated region. The ORF codes for a protein consisting of 467 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 13 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 52 kDa that was almost identical with the molecular weight of 54,065 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 57 kDa which is considered to have a sugar chain being attached after secretion. In addition, there exist in the amino acid sequence of this protein three sites at which N-glycosylation may occur (Asn-Arg-Thr at position 171, Asn-Ser-Thr at position 239 and Asn-Asp-Thr at position 377). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from histidine at position 29. When expressed in COS7 cells, an expression product of about 55 kDa was observed in the supernatant fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human α -L-fucosidase (SWISS-PROT Accession No. P04066). Table 8 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human α -L-fucosidase (FC). Therein,

the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both
 5 proteins shared a homology of 54.8% in the entire region.

Table 8

	HP	MRPQELPRLAFPLLLLLLLLLLPPPPC-PAHSATRFDPTWESLDARQLPAWFDQAKFGIFI
10		.*****.* .. . *... *...* ***.*.....*****.*
	FC	MRSRPAGPALLLLLLLFLGAAESVRRRAQPPRRYTPDWPSLDSRPLPAWFDEAKFGVFI
	HP	HWGVFSVPSFGSEFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWAD
		*****.*.....** * *.* ***.*.....*.*.....**.*.....*
	FC	HWGVFSVPAWGSEFWWHWQGEGRPQYQRFMRDNYPGFSYADFGPQFTARFFHPEEWAD
15	HP	IFQASGAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFLG
		.***.*.....*.....** * *****. * ***.*.....*.....*
	FC	LFQAAGAKYVVLTTKHHEGFTNWSPVSWNWSKDVGPHRDLVGELGTALRR-NIRYGL
	HP	YYSLFEFWFHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWN
		..*.....* *.....*.....*.....*.....*.....*.....*.....*
20	FC	YHSLLEWFHPLYLLDKNGFKTQHVFSAKTMPELYDLVNSYKPDLIWSDGEWECPDITYWN
	HP	STGFLAWLYNESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDK
		**.*.*.....*.....*.....*.....*.....*.....*.....*.....*
	FC	STNFLSWLYNDSPVKDEVVNDRWGQNCSSCHGGYINCEDKFKPQSLPDHKWEMCTSIDK
	HP	LSWGYRREAGISDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQMGSW
25		.*****.*.....*.....*.....*.....*.....*.....*
	FC	FSWGYRRDMALSDVTEESEIISELVQTVSLGGNYLLNIGPTKDGILVPIFQERLLAVGKW
	HP	LKVNGEAIYETHTWRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGA
	*.....*.....*.....*.....*.....*.....*
	FC	LSINGEAIYASKPWRVQWEKNTTSVWYTSKGS--VYAIFLHWPENGVLNLESPITT-ST
30	HP	TEVKLLGHGQPLNWISLEQNGIMVELPQLTIHQMPCKKGWALALTNVI
	*.....*.....*.....*.....*.....*
	FC	TKITMLGIQGDLKWSTDPDKGLFISLPQLPPSAVPAEFAWTIKLTGVK

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N28668) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

10 <HP10357> (SEQ ID Nos. 34, 44, and 54)

Determination of the whole base sequence of the cDNA insert of clone HP10357 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 113-bp 5'-untranslated region, a 300-bp ORF, and a 54-bp 3'-untranslated region. The ORF codes for a protein consisting of 99 amino acid residues and there existed two putative transmembrane domains. Figure 14 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 11 kDa that was almost identical with the molecular weight of 10,923 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA477156) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

30 <HP10447> (SEQ ID Nos. 35, 45, and 55)

Determination of the whole base sequence of the cDNA

insert of clone HP10447 obtained from cDNA library of human liver revealed the structure consisting of a 271-bp 5'-untranslated region, a 570-bp ORF, and a 34-bp 3'-untranslated region. The ORF codes for a protein consisting of 189 amino acid residues and there existed five putative transmembrane domains. Figure 15 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA296976) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10477> (SEQ ID Nos. 36, 46, and 56)

Determination of the whole base sequence of the cDNA insert of clone HP10477 obtained from cDNA library of human liver revealed the structure consisting of a 149-bp 5'-untranslated region, a 1092-bp ORF, and a 15-bp 3'-untranslated region. The ORF codes for a protein consisting of 363 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 16 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 40 kDa that was almost identical with the molecular weight of 39,884 predicted from the ORF.

The search of the protein data base using the amino

Table 9

```

15  HP MVDSLLAVTLAGNLGLTFLRGSQTQSHPDLGTEGCWDQLSAPRTFTLLDPKASLLTKAFL
    HP NGALDGVILGDYLSRTPEPRPSLSHLLSQYYGAGVARDPGFRSNFRRQNGAALTSASILA
    HP QQVWGTLVLLQRLEPVHLQLQCMSQEQLAQVAANATKEFTEAFLGCPAHPRCRWGAAPY
                                     *..* ** * * .

    PG                MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALA-
20  HP RGRPKLLQLPLGFLYVHHTYVPAPPCTDFTRCANMRSMQRYHQDTQGWGDIGYSFVVGS
    .. .. * *** .. * ** .....*.. ..*... *...** . * ** *...*...
    PG SECAQHLSLPLRYVVVSHT--AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGE
    HP DGYVYEGRGWHWVGAHTLGH-NSRGGFVAIVGNYYAALPTEAALRTVRDTLPSCAVRAGL
    ** *****.....** . *.....** . ** ..... * .** . *
25  PG DGLVYEGRGWNFTGAHSGHLWNPMSIGISFMGNYMDRVPTPQAIRAAQGLL-ACGVAQGA
    HP LRPDYALLGHRQLVRTDCPGDALFDLLRTWPHFTATVKPRPARSVSKRSRREPPPRTLPA
    **...* *... ..** .....*...*...*...
    PG LRSNYVLKGHRDVORTLSPGNOLYHLIONWPHYRSP

```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration

of sequences that shared a homology of 90% or more (for example, Accession No. AA424759) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10513> (SEQ ID Nos. 37, 47, and 57)

Determination of the whole base sequence of the cDNA insert of clone HP10513 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 134-bp 5'-untranslated region, a 750-bp ORF, and a 0-bp 3'-untranslated region. The ORF codes for a protein consisting of 249 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 17 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 29 kDa that was almost identical with the molecular weight of 27,373 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human hypothetical protein KIAA0512 (GenBank Accession No. AB011084). Table 10 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human hypothetical protein KIAA0512 (KI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 31.6% in the C-terminal region of 196 amino acid residues.

Table 10

```

5      HP                                     MGGRGAGWVAAGLLLGAGACYCIYRLTRGRRRG

      KI RGRGRRPVAMQKRPFYPYEIDEILGVRDLRKVLALLQKSDDPFIQQVALLTSLNNANYSCN
      HP DRELGIRSSKSAEDLTDGSYDDVLNAEQLQKLLYLLESTEDPVIIERALITLGNNAAFSV
                                     *   . . . . *   .   * * . * . .   . . . .   *
      KI QETIRKLGGLPPIANMINKTDPHIKEKALMAMNNLSENYENQGRLOVYMNKVMDDIMASN
10     HP NQAIIRELGGIPIVANKINHSNQSISKEKALNALNNLSVNVENQIKIKVQVLKLLLNLSEN
      . . . . *   . . . . * .   . . . .   . .   . .   ***** * . * . * . *
      KI LNSAVQVVGKFLTNMTITNDYQHLLVNSIANF--FRLLSQGGGKIKVEILKILSNFAEN
      HP PAMTEGLLRAQVDSSFLSLYDSHVAKEILLRVLTFLQNIKNCLKIEGHLAVQPTFTEGSL
      * . *   * . . . * . * . * . * . * . . . * . *   .   . . . . * . *
15     KI PDMLKKLLSTQVPASFSSLYNSYVESEILINALTLFEIIYDNLRAE--VFNYREFNKGSL
      HP FFL-LHGEECAQKIRALVDHHDAAEVKEKVVTIIPKI
      * . *   . .   * . . * . . . * . . * . *   * . . . .   * .
      KI FYLCTTSGVCVKKIRALANHHDLLVKVKVIKLVNKF

```

20 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. N92228) in ESTs, but, since they are
25 partial sequences, it can not be judged whether or not any
of these sequences codes for the same protein as the protein
of the present invention.

<HP10540> (SEQ ID Nos. 38, 48, and 58)

30 Determination of the whole base sequence of the cDNA
insert of clone HP10540 obtained from cDNA library of human
osteosarcoma cell line Saos-2 revealed the structure

consisting of a 47-bp 5'-untranslated region, a 297-bp ORF, and a 245-bp 3'-untranslated region. The ORF codes for a protein consisting of 98 amino acid residues and there existed two putative transmembrane domains. Figure 18 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CEF49C12.12 (GenBank Accession No. Z68227). Table 11 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein CEF49C12.12 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 36.1% in the entire region.

Table 11

25	HP M-ASLLCCGPKLAACGIVLSAWGVIMLIMLGIFFNVHSAVLIEDVPFTEKDFENGPNQNIY
	* *** * * * * * * * * * * * *
	CE MGKICPLMGPKMSAFCMVMSVWGVIFLGLLGVFFYIQAVTLFPDLHF-EGHGKVPSSVID
	HP NLYEQVSYNCFIAAGLYLLLGGFSFCQVRLNKRKEYMVR
	* * * * * * * * * *
30	CE AKYNEKATQCWIAAGLYAVTLIAVFWQ---NKYNTAQIF

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA420715) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

10 <HP10557> (SEQ ID Nos. 39, 49, and 59)

Determination of the whole base sequence of the cDNA insert of clone HP10557 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 24-bp 5'-untranslated region, a 519-bp ORF, and a 130-bp 3'-untranslated region. The ORF codes for a protein consisting of 172 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 19 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 32 kDa that was larger than the molecular weight of 18,844 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 39 kDa which is considered to have been subjected to some modification after secretion. In addition, there exist in the amino acid sequence of this protein no site at which N-glycosylation may occur. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 32. When expressed in COS7 cells, an expression product of about 20 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human progesterone binding protein (EMBL Accession No. AJ002030). Table 12 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human progesterone binding protein (PG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 30.5% in the C-terminal region of 151 amino acid residues.

Table 12

15	HP	MVGPA
	<hr/>	
	PG MAAGDGDVKGTLGSGSESSNDGGSESPGDAGAAEGGGWAAAALALLTGGGEMLLNVAL	
	HP RRRRLRPLAALALVLALAPGLPTARAGQTPRPAERGPPV--RLFTEEEELARYGGEEEDQPI	
20	** * . . . * . * . . . * *	
	PG VALVLLGAYRLWVRWGRRGLGAGAGAGEESPATSLPRMKKRDFSLEQLRQYDG-SRNPRI	
	HP YLAVKGVVFDVTSKGFEFYGRGAPYNALTGKDSTRGVAKMSLDPADLTHDTTGLTAKELEA	
	. * **. * * * *	
	PG LLAVNGKVFDVTKGSKFYGPAGPYGIFAGRDA SRGLATFCLDKDALRDEYDDLSDLNAVQ	
25	HP LDEV--FTKVYKAKYPIVGYTARRILNEDGSPNLDKPEDQPHFDIKDEF	
	... * * * * * *	
	PG MESVREWEMQFKEKY---DYVG-RLLKPGEEPS-EYTDEEDTKDHNKQD	
	<hr/>	

30 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. AA101709) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

5

<HP10563> (SEQ ID Nos. 40, 50, and 60)

Determination of the whole base sequence of the cDNA insert of clone HP10563 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure
10 consisting of a 126-bp 5'-untranslated region, a 363-bp ORF, and a 936-bp 3'-untranslated region. The ORF codes for a protein consisting of 120 amino acid residues and there existed two putative transmembrane domains. Figure 20 depicts the hydrophobicity/hydrophilicity profile, obtained
15 by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 18.5 kDa that was larger than the molecular weight of 13,180 predicted from the ORF.

The search of the protein data base using the amino
20 acid sequence of the present protein revealed that the protein was similar to the Arabidopsis thaliana hypothetical protein F27F23.15 (GenBank Accession No. AC003058). Table 13 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the A.
25 thaliana hypothetical protein F27F23.15 (AT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins
30 shared a homology of 35.5% in the entire region.

Table 13

```

HP MMPSRTNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIALATVLFLLIGAFLLI
      *...* * . . . . * *.**.*. *...* *
5  AT          MAYVDHAFSISDEDLMIGTSY-TVSNRPPVKEISLAVGLLVFGTLGI
HP IIGSLLLSGYISKGGADRAVPVLIIGILVFLPGFYHLRIAYYASKGYRGYSYDDIPDFDD
      ..* .. . . . *. . . . . . . * *.**.*. . . . . . . . . . . . . . . . .
AT VLGFFMAYNRVG-GDRGHGIFFIIVLGCLLFIPGFYYTRIAYYAYKGYKGFSFSNIPSV

```

10

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA083574) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP01467> (SEQ ID Nos. 61, 71, and 81)

20 Determination of the whole base sequence of the cDNA insert of clone HP01467 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 65-bp 5'-untranslated region, a 924-bp ORF, and a 447-bp 3'-untranslated region. The ORF codes for a

25 protein consisting of 307 amino acid residues and there existed three putative transmembrane domains. Figure 21 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation

30 product of high molecular weight.

The search of the protein data base using the amino

acid sequence of the present protein revealed that the protein was similar to the rat Sec22 homologue (GenBank Accession No. U42209). Table 14 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the rat Sec22 homologue (RN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 94.6% in the N-terminal region of 241 amino acid residues. The protein of the present invention was longer by 53 amino acids at the C-terminus than the rat Sec22 homologue.

15

Table 14

	HP	MSMILSASVIRVRDGLPLSASTDYEQSTGMQECRKYFKMLSRKLAQLPDRCTLKTGHYNI
		*****.*****.***.*.*****.*****..**
	RN	MSMILSASVVRVRDGLPLSASTDCEQSAGVQECRKYFKMLSRKLAQFPDRCTLKTGRHNI
20	HP	NFISSLGVS YMMMLCTENYPNVLA FSFLDELQKEFITTYNMMKTNTAVRPYCFIEFDNFIQ

	RN	NFISSLGVS YMMMLCTENYPNVLA FSFLDELQKEFITTYNMMKTNTAVRPYCFIEFDNFIQ
	HP	RTKQRYNNPRSLSTKINLSDMQTEIKLRPPYQISMCELGSANGVTSAFSVDCKGAGKISS
		*****.*****.*****
25	RN	RTKQRYNNPRSLSTKINLSDMQMEIKLRPPYQIPMCELGSANGVTSAFSVDCKGAGKISS
	HP	AHQRLPATLSGIVGFILSLLCGALNLIRGFHAIESLLQSDGDDFNYYIAFFLGTAACLY
		*****.*****.***.*.*****
	RN	AHQRLPATLSGIVAFILSLLCGALNLIRGFHAIESLLQSDGEDFSYIMIAFFLGTAACLY
	HP	QCYLLVYYTGWRNVKSFLT FGLICLCNMYLYELRN LWQLFFHVTVGAFVTLQIWL RQAQG
30		*
	RN	QMICLC LQGRKERT

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA421925) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP01956> (SEQ ID Nos. 62, 72, and 82)

Determination of the whole base sequence of the cDNA insert of clone HP01956 obtained from cDNA library of human liver revealed the structure consisting of a 86-bp 5'-untranslated region, a 552-bp ORF, and a 359-bp 3'-untranslated region. The ORF codes for a protein consisting of 183 amino acid residues and there existed one putative transmembrane domain. Figure 22 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 20.5 kDa that was almost identical with the molecular weight of 20,073 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the yeast hypothetical protein 21.5 kDa (SWISS-PROT Accession No. P53073). Table 15 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the yeast hypothetical protein 21.5 kDa (SC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology

of 34.3% in the C-terminal region of 108 amino acid residues.

Table 15

5	<p>HP MTAQGGLVANRGRFRKWAIELSGPGGSRGRSDRGSGQGDSLVPVGYLDKQVPDTS</p> <p>SC MSEQEPYEWAKHLLDTKYIEKYNIQNSNTLPSPPGFEGNSSKGNVTRKQQDATSQTTSLA</p> <p>HP VQETDRILVEKRCWDIALGPLKQIPMNLFIMYMAGNTISIFPTMMVCMMAWRPIQALMAI</p> <p style="padding-left: 40px;">.* .. *.*.* * * *.*.*.* *.*.*.* *.*.*.* *.*.*.*</p>
10	<p>SC QKNQITVLQVQKAWQIALQPAKSIPMNIFMSYMSGTSLQIIPIMTALMLLSGPIKAIFST</p> <p>HP SATFK--MLESSSQKFLQGLVYLIGNLMGLALAV-Y-KCQSMGLLPTHASDWLAFIEPPE</p> <p style="padding-left: 40px;">...***.*.*. * . . . * * .*****.*.</p> <p>SC RSAFKPVLGNKATQSQVQTAMFMYIVFQGVLMYIGYRKLNSMGLIPNAKGDWLPWERIAH</p> <p>HP RMEFSGGGLLL</p>
15	<p>SC YNNGLQWFSD</p>

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA159753) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02545> (SEQ ID Nos. 63, 73, and 83)

Determination of the whole base sequence of the cDNA insert of clone HP02545 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 133-bp 5'-untranslated region, a 984-bp ORF, and a 636-bp 3'-untranslated region. The ORF codes for a

protein consisting of 327 amino acid residues and there
existed a putative secretory signal at the N-terminus and
one putative transmembrane domain at the C-terminus. Figure
23 depicts the hydrophobicity/hydrophilicity profile,
5 obtained by the Kyte-Doolittle method, of the present
protein.

The search of the protein data base using the amino
acid sequence of the present protein revealed that the
protein was similar to the rat embigin (EMBL Accession No.
10 AJ009698). Table 16 shows the comparison between amino acid
sequences of the human protein of the present invention (HP)
and the rat embigin (RN). Therein, the marks of -, *, and .
represent a gap, an amino acid residue identical with that
of the protein of the present invention, and an amino acid
15 residue similar to that of the protein of the present
invention, respectively. The both proteins shared a homology
of 65.4% in the entire region.

Table 16

```

HP MRALPGLLEARARTPRLLLLQCLLAAARPSSADGSAPDSPFTSPPLREEIMAN--NFSLE
  ** . ** . * . . ***** . ***** . ***** . ***** . *****
5 RN MRSHTGLRALVAPGCSLLLL-YLLAATRPDRAVGDPADSAFTSLPVREEMMAKYANLSLE
HP SHNISLTEHSSMPVEKNITLERPSNVNLTCQFTTSGDLNAVNVTWKKDGEQLE--NNYLV
  . ***** . ***** . ***** . ***** . ***** . *****
10 RN TYNISLTEQTRVS-EQNITLERPSHLELECTFTATEDVMSMNVTWKKDDALLETTDGFNT
HP SATGSTLYTQYRFTIINSKQMGSYSCFFREEKEQRGTFNFKVPELHGKNKPLISYVGDST
  . * . ***** . ***** . ***** . ***** . ***** . *****
15 RN TKMGDTLYSQYRFTVFNSKQMGKYSCFLGEE--LRGTFNIRVPKVHGKNKPLITYVGDST
HP VLTCKCQNCFPLNWTWYSSNGSVKVPVGVQM-NKYVINGTYANETKLKITQILLEEDGESY
  * . * . ***** . ***** . ***** . ***** . ***** . *****
RN VLKCECQNCPLNWTWYMSNGTAQVPIDVHVNDKFDINGSYANETKLKVHLLLEEDGGSY
15 HP WCRALFQLGESEEHIELVVLVPLKPFVIVAEVILLVATILLCEKYTQKKKKHSDEG
  ***** . ***** . ***** . ***** . ***** . ***** . *****
RN WCRAAFPLGESEEHKLVVLSFMVPLKPFVIVAEVILLVATILLCEVYTQKKKNDPDDG
HP KEFEQIEQLKSDDSDNGIENNVPRHRKNESLGQ
  ***** . ***** . ***** . ***** . ***** . ***** . *****
20 RN KEFEQIEQLKSDDSDNGIENNVPRYRKTDSDGQ

```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA312629) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02551> (SEQ ID Nos. 64, 74, and 84)

Determination of the whole base sequence of the cDNA insert of clone HP02551 obtained from cDNA library of human

osteosarcoma cell line Saos-2 revealed the structure consisting of a 61-bp 5'-untranslated region, a 672-bp ORF, and a 384-bp 3'-untranslated region. The ORF codes for a protein consisting of 223 amino acid residues and there
5 existed a putative secretory signal at the N-terminus. Figure 24 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was somewhat larger than
10 the molecular weight of 24,555 predicted from the ORF. In this case, the addition of a microsomal led to the formation of a product of 26 kDa from which the secretory signal is considered to have been cleaved. Application of the (-3,-1) rule, a method for predicting the cleavage site of the
15 secretory signal sequence, allows to expect that the mature protein starts from glutamine at position 20.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse FGF binding protein
20 (GenBank Accession No. U49641). Table 17 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse FGF binding protein (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the
25 protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 21.2% in the entire region other than the N-terminal region. In particular, all the eight cysteine residues contained in the
30 both proteins were conserved.

Table 17

	HP	MKFVPCLLLVTLSCLGTLGQAPRQKQGST
		...*. . .*
5	MM	MRLHSLILLSFLLLATQAFSEKVRKRAKNAPHSTAEEGVEGSAPSLGKAQNQRSRTSKS
	HP	GEEFHFQTGGRDSCMRPSSLGQGAGEVWLRVDCRNTDQTYWCEYRGQPSMCQAFADPK
		..* ** * * *
	MM	LTHGKFVTKDQATC---RWAVTEEEQGISLKVQCTQADQEFSCVFAGDPTDCLKHDKD-Q
	HP	SYWNQALQELRRLHHACQGA-PVLRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTP
10		***.* * * *
	MM	IYWKQVARTLRKQKNICRDAKSVLKTRVCRKRFPESNLKLVPNARGNTKPRKEKAEVSA
	HP	SLRPKATVKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAKKAWEHWCWK
		. . * * * *
	MM	REHNKVQEA VSTEPNRIKEDI-TLNPAATQTM-TIRDPECLEDPDVLNQ-RKTALEFCGE
15	HP	PFQALCAFLISFFRG
	*
	MM	SWSSICTFFLNMLQATSC

20 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA317400) in ESTs, but, since they are partial sequences, it can not be judged whether or not

25 any of these sequences codes for the same protein as the protein of the present invention.

<HP02631> (SEQ ID Nos. 65, 75, and 85)

30 Determination of the whole base sequence of the cDNA insert of clone HP02631 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 42-bp 5'-untranslated region, a 147-bp ORF,

and a 1191-bp 3'-untranslated region. The ORF codes for a protein consisting of 48 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 25 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa or less.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA156969) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02632> (SEQ ID Nos. 66, 76, and 86)

Determination of the whole base sequence of the cDNA insert of clone HP02632 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 50-bp 5'-untranslated region, a 1116-bp ORF, and a 337-bp 3'-untranslated region. The ORF codes for a protein consisting of 371 amino acid residues and there existed eight putative transmembrane domains. Figure 26 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CELC2H12 (GenBank Accession No. U23169). Table 18 shows the comparison between amino acid sequences

Table 18

```

HP MAWTKYQLFLAGLMLVTGSLNTLSAKWADNFMAEGCGGSKEHSFQHPFLQAVGMFLGEFS
      ..... *.*****.***.*****..... . *.*****. ***.***
CE MVAFAVIISVMMVVTGSLNTICAKWADSIKAD-----GVPFNHPFLQATCMFFGEFL
HP CLAAFYL-----LRCRAAGQSDS-----SVDPQQPFNPFLFLPPALCDMTGTSL
      ***.***      * ...*.***      . . *.*****.***.
CE CLVVFFLIFGYKRYVWNRANVQGESGSVTEITSEEKPTLPPFNPFLEFFPALCDILGTSI
HP MYVALNMTSASSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWLGLATIAGLVVVGGLADLL
      ***.***.***.*****.*****.***.***. . . *.***. . ***.***.
CE MYIGLNLTTASSFQMLRGAVIIFTGLLSVGMLNAQIKPFWFGMLFVMLGLVIVGVTDIY
HP SKHDSQHKLSEVITGDLII IMAQII VAIQMVLEEKFVYKHNHPLRAVGTEGLFGFVILS
      ...* . . .***.***.*****.***.***. *...*.***.***.***.***.***
CE YDDDPLDDKNAIITGNLLIVMAQII VAIQMVEEQKYLTKYDVPALFAVGLEGLFGMVTLS
HP LLLVPMYYIPAG-SFSGNPRGTLEDALDAFCQVGQOPLIAVALLGNISSIAFFNFAGISV
      *.***.***.***.***.***.***.***.***.***.***.***.***.***.***
CE ILMIPFYYIHVPRTFSTNPEGRLEDVFYAWKEITEEPTIALALSGTVVSI AFFNFAGVSV
HP TKELSATTRMVLDLRTTVI WALSLALGW EAFHALQILGFLILLIGTALYNGLHRPLLGR
      *****.***.***.***.***.***.***.***.***.***.
CE TKELSATTRMVLDL SVRTLVIWVVS IPLFHEKFIAIQLSGFAMLILGTLIYNDILIGPWFR
HP LSRGRPLAESEQERLLGGTRTPINDAS
CE RNILPNLSSHANCARCWLCICGGDSELIEYEQEDOEHLMEA

```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N50907) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10488> (SEQ ID Nos. 67, 77, and 87)

Determination of the whole base sequence of the cDNA insert of clone HP10488 obtained from cDNA library of human liver revealed the structure consisting of a 39-bp 5'-untranslated region, a 273-bp ORF, and a 421-bp 3'-untranslated region. The ORF codes for a protein consisting of 90 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 27 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was almost identical with the molecular weight of 10,151 predicted from the ORF. When expressed in COS7 cells, an expression product of about 6 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H73534) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10538> (SEQ ID Nos. 68, 78, and 88)

Determination of the whole base sequence of the cDNA insert of clone HP10538 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 357-bp 5'-untranslated region, a 1500-bp ORF, and a 1911-bp 3'-untranslated region. The ORF codes for a protein consisting of 499 amino acid residues and there existed at least four putative transmembrane domains. Figure 28 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse pore-forming K⁺ channel subunit (GenBank Accession No. AF056492). Table 19 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse pore-forming K⁺ channel subunit (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 32.4% in the N-terminal region of 241 amino acid residues.

Table 19

```

HP  MVDRGPLLLTSAIIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFPCLGQEGLDK
      * . . . . . * . * . . . . . * . . . . . * . . . . . * . . . . .
5  MM  MRSTLLALLALVLLYLVS GALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED
HP  ILEVVS DAAGQG-----VAITGNQTFNWNWPNAMIFAATVITTIGYGNVAPKTPAGRLE
      . . . . . * * * . . . . . * . * . . . . . * . . . . . * . . . . .
MM  FIKLLVEALGGGANPETS WTNSSNHSSAWNLSGAFFFSGTIITIGYGNIVLHTDAGRLE
HP  CVFYGLFGVPLCLTWISALGKFFGGRAKR----LGQFLTKRGVSLRKAQITCTVIFIVWG
10  * . . . . * . . . . . * . . . . . * . . . . . * . . . . . * . . . . .
MM  CIFYALVGIPPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLLIG
HP  VLVHLVIPPFVFMVTEGWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELW
      * . . . . * . . . . . * . . . . . * . . . . . * . . . . . * . . . . .
MM  CLLFVLTPFTFVFSYME SWSKLEAIYFVIVTLTTVGF GDYVPG-DGTGQNSPAYQPLVWF
15  HP  IYLG L AWSLFLVNWKVSMFVEVHKAIKRRRRRRKESFESSPHSRKALQVKGSTASKDVNI
      * . . . . .
MM  ILFGLAYFASVLT TIGNWLRAVSRRTAEMGGLTAQAASWTGTVTARVTQRTGPSAPPPE

```

20 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. R25184) in ESTs, but, since they are
partial sequences, it can not be judged whether or not any
25 of these sequences codes for the same protein as the protein
of the present invention.

<HP10542> (SEQ ID Nos. 69, 79, and 89)

30 Determination of the whole base sequence of the cDNA
insert of clone HP10542 obtained from cDNA library of human
stomach cancer revealed the structure consisting of a 23-bp
5'-untranslated region, a 321-bp ORF, and a 426-bp 3'-

untranslated region. The ORF codes for a protein consisting of 106 amino acid residues and there existed one putative transmembrane domain. Figure 29 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,724 predicted from the ORF. When expressed in COS7 cells, an expression product of about 13 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA029683) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10571> (SEQ ID Nos. 70, 80, and 90)

Determination of the whole base sequence of the cDNA insert of clone HP10571 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 95-bp 5'-untranslated region, a 459-bp ORF, and a 675-bp 3'-untranslated region. The ORF codes for a protein consisting of 152 amino acid residues and there existed one putative transmembrane domain. Figure 30 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 20 kDa that was larger than the molecular weight of 17,062 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 23 kDa

which is considered to have a sugar chain being attached after secretion. In addition, there exists in the amino acid sequence of this protein one site at which N-glycosylation may occur (Asn-Ile-Thr at position 10).

5 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA105822) in ESTs, but, since they are partial sequences, it can not be judged whether or not
10 any of these sequences codes for the same protein as the protein of the present invention.

<HP01470> (SEQ ID Nos. 91, 101, and 111)

15 Determination of the whole base sequence of the cDNA insert of clone HP01470 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 157-bp 5'-untranslated region, a 1077-bp ORF, and a 385-bp 3'-untranslated region. The ORF codes for a protein consisting of 358 amino acid residues and there existed one putative
20 transmembrane domain. Figure 31 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 43 kDa that was somewhat larger than the molecular weight
25 of 40,489 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 40 kDa from which the secretory signal is considered to have been cleaved and a product of 43.5 kDa which is considered to have been subjected to some modification. Application of the
30 (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 23. When

expressed in COS7 cells, an expression product of about 44 kDa was observed in the supernatant fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein 39.9 kDa (SWISS-PROT Accession No. Q10005). Table 20 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein 39.9 kDa (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 58.9% in the entire region.

Table 20

```

HP MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDD
      *.. * *****...* ..***** .*****.**
5 CE MRILNVSLVLASSLVAFVECGRDFYKILGVAKNANANQIKKAYRKLAKELHPDRNQDD
HP PQAQEKFDLGAAYEVLSDEKRRQYDTYGEGL--KDGHQSSHGDIFSHFFGDFGFMFG
      *.*****.*****.*** ** .****. ..* .. * ** ***** *
CE EMANEKFQDLSSAYEVLSDEKRAMYDRHGEEGVAKMGGGGGGGHDPFSSFFGDF-FG-G
HP GTPRQQDRNIPRGSIIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTT
10      *. . . .*.*.*** *****.****. *.*. * ..*.****.****.
CE GGGHGGEETPKGADVITIDLFVTLEEVYNGHFVEIKRKKAVYKQTSQTRQCNCRHEMRTE
HP QLGPGRFQMTQEVVCECPNVKLVNEERTLEVEIEPGVRDGMETPFIFEGEGEPHVDGEPGD
      *.***** * *****.*.....* * . * . * *****.*.***
CE QMGQGRFQMFQVKVCECPNVKLVQENKVLVEVEVEVGADNGHQQIFHGEGERPHIEGDPGD
15 HP LRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAK
      *.*.*. *** *.*****.*** * ..* ***** * .. ***.*.***.
CE LKFKIRIQKHPRFERKGGDDLYTNVTISLQDALNGFEMEIQHLDGHIVKVQORDKVTWPGAR
HP LWKKGEGLPNFDNKNKIGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQ-KVYNGLQG
      *.***.*.***.*** ** *..*****.***.....* ..*.....* .*****
20 CE LRKKDEGMPSLEDNNKKGMLVVTDFDVEFPKTELSDEQKAQIIIEILQONTVKPKAYNGL

```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA282838) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

30 <HP002419> (SEQ ID Nos. 92, 102, and 112)

Determination of the whole base sequence of the cDNA insert of clone HP02419 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 253-bp

5'-untranslated region, a 681-bp ORF, and a 1120-bp 3'-untranslated region. The ORF codes for a protein consisting of 226 amino acid residues and there existed four putative transmembrane domains. Figure 32 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human hypothetical protein KIAA0108 (SWISS-PROT Accession No. Q15012). Table 21 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human hypothetical protein KIAA0108 (KI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.9% in the entire region.

Table 21

HP MKMVPWPWTRFYSNSCLCCHVRTGTTILLGVWYLIINAVLLILLSALADPD---QY
 *****.
 5 KI MVSMSFKRNRSDRFYSTRCCGCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPN SMPAV
 HP NFSSELGGDFEF-MDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDF
 *.
 KI NIQYEVIGNYYSSERMADNACVLFVSVLMFIISSMLVYGAISYQVGWLIIPFFCYRLFDF
 HP ALNMLVAITVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFFKGYL
 10 *.
 KI VLSCLVAISSLTYPRIKEYLDQL-PDFPYKDDLALDSSCLLFIVLVFFALFIIFKAYL
 HP ISCVWNCYRYINGRNSSDVLVYVT-SNDTTVLLPPYDDATVNGAAKEPPPPYVSA
 *.
 KI INCVWNCYKYINNRNVPEIAVYPAFEAPPQYVLPTY-EMAVKMPEKEPPPPYLP

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA173214) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

25 <HP02631> (SEQ ID Nos. 93, 103, and 113)

Determination of the whole base sequence of the cDNA insert of clone HP02631 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 42-bp 5'-untranslated region, a 588-bp ORF, and a 750-bp 3'-untranslated region. Although the 49th amino acid residue is encoded by a stop codon, it is likely that this codon encodes selenocysteine from the molecular weight

of the translation product and the sequence comparison data with the *Caenorhabditis elegans* homologue. The ORF codes for a protein consisting of 195 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the intermediate region. Figure 33 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 58 kDa. In this case, the addition of a microsome led to the formation of a product of 56 kDa from which the secretory signal is considered to have been cleaved. Since both of these products are larger than the molecular weight of 22 kDa predicted from the ORF, it is likely that the protein interacts with another protein.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein C35C5.3 (EMBL Accession No. Z78417). Table 22 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein C35C5.3 (CE). U at position 49 in the amino acid sequence of the protein of the present invention represents selenocysteine. Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 37.9% in the entire region other than the N-terminal region. Cystein was found in the sequence of the *C. elegans* protein at the position corresponding to position 49 encoded by the stop codon (selenocysteine) of the protein of the present invention.

Table 22

	HP	MRLLLL
--	----	--------

5	CE MRIHDELQKDMSRFGVFIIGVLEFFMSVCDVLRTEESHSHDENHVHEKDDFEAEFGDETDS
	HP LLVAASAMVRSEASANLGGVPSKRLKMQYATGPLLKQICVSUGYRRVFEEYMRVISQRY
	* *.. *** **..... *
	CE QSFSQGTEEDHIEVREQSSSVKPTAVHHAKDLPTLRIFYCVSCGYKQAFDQFTTFAKEY
	HP PDIRIEGENYLPQPIYRHIAFLSVFKLVLIIGLIIVGKDPFAFFGMQAPSIWQWGQENKV
10	*...***.*. * ..* ** *.... *.. * .***. **. * * *
	CE PNMPIEGANFAPVLWKAYVAQALSFKMAVLVLVLGGINPFERFGLGYPQILQHAHGNKM
	HP YACMMVFFLSNMIENQCMSTGAFEITLNDVPVWSKLESGLPSMQQLVQILDNEMKLNH
	.***.***.*..... .*****. *.. ..*****.*** *.....
	CE SSCMLVFMLGNLVEQSLISTGAFEVYLGNEQIWSKIESGRVPSPQEFMQLIDAQLAVLGK
15	HP MDSIPHHR

CE APVNTESFGEFQQT

20 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA156969) in ESTs, but, since they are partial sequences, it can not be judged whether or not

25 any of these sequences codes for the same protein as the protein of the present invention.

<HP02695> (SEQ ID Nos. 94, 104, and 114)

30 Determination of the whole base sequence of the cDNA insert of clone HP02695 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 112-bp 5'-untranslated region, a 1020-bp ORF, and a 160-bp 3'-

untranslated region. The ORF codes for a protein consisting of 339 amino acid residues and there existed three putative transmembrane domains. Figure 34 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 38 kDa that was almost identical with the molecular weight of 38,274 kDa predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the rat hypertension-induced protein S-2 fragment (PIR Accession No. 539959). Table 23 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the rat hypertension-induced protein S-2 fragment (RN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 74.3% in the entire region.

Table 23

HP MNWELLLWLLVLCALLLLLVQLLRFLRADGDLTLLWAEWQGRRPEWELTDMVVWVTGASS

5 HP GIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLLENGNLKEKDILVLPLDLTDTGSHEA
 *****.*****.***.***.
 RN VKRRSLENGNLKEKDILVLPLDLADTSSHDI
 HP ATKAVLQEFGRIDILVNNGGMSQRSCLMDTSLDVYRKLIELNYLGTVSLTKCVLPHEMER
 .**... ** .*...***.***** ****.*

10 RN ATKTVLQEFGRIDILVNNGGVAHASLVENTNMDIFKVLIEVNYLGTVSLTKCFLPHMMER
 HP KQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGPVQSN
 .*****...*
 RN NQGKIVVMKS

15

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T84331) in ESTs, but, since they are

20 partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10031> (SEQ ID Nos. 95, 105, and 115)

25

Determination of the whole base sequence of the cDNA insert of clone HP10031 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 55-bp 5'-untranslated region, a 1464-bp ORF, and a 649-bp 3'-untranslated region. The ORF codes for a

30 protein consisting of 487 amino acid residues and there existed eleven putative transmembrane domains. Figure 35 depicts the hydrophobicity/hydrophilicity profile, obtained

by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight. When expressed in COS7 cells, an expression product of about 55 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CELK07H8 (GenBank Accession No. AF047659). Table 24 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein CELK07H8 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 44.2% in the entire region.

Table 24

```

HP                                MDGTETRQRRRLDSCGKPGELGLPHPLSTGGLPVAS

5  CE MKGGGGIGDGKKDYQSAVHEGLTTTFDQLGIALEDVGKSMDAETATPGGSLFSRVIFRFRN
HP EDGALRAPESQSVTPKPLETEPSRETAWSIGLQVTVPFMFAGLGLSWAGMLLDYFQHPV
   *...*..... . . . . *... . ** ** ***** .***... **
CE ENSSLKSRTYDHSNDLVNMSVIPAESSVVLFFQVLPFAVAGLGMVFAVLVLSIVVTWPL
HP FVEVKDLLTLVPPLVGLKGNLEMTLASRLSTAANTGQIDDPQEQHRVISSNLALIQVQAT
10  * * . ...*****.*.....** *...*.....* . *****.*****
CE FEEIPEILILVPALLGLKGNLEMTLASRLSTLANLGHMDSSKQRKDVVIANLALVQVQAT
HP VVGLLAAVAALLLGVVSREEVDVAKVELLCASSVLTAFLAALFALGVLVCIVIGARKLGV
   **..**.. * * . .... * * . *.*****. ** *...*.....** ..
CE VVAFLASAFAAALAFIPSGDFDWAHGALMCASSLATAACSASLVLSLLMVVIVTSRKYNI
15  HP NPDNIATPIAASLGDLITLSILALVSSFFYR--HKDSRYLTPLVCLSF AALTPVWVLI AQ
   ****.*****.***...*. * * . *.....* . * . * * * * . **..
CE NPDNVATPIAASLGDLTTLTVLAFFGSVFLKAHNTESWLVNIVIVLFLLLLFPWIKIANE
HP SPPIVKILKFGWFPIILAMVISSFGGLILSKTVSKQQYKGMAIFTPVICGVGGNLVAIQT
   . . ..* ** *...*.*** **.....* ..*.....** *****.***.
20  CE NEGTOETLYNGWTPVIMSMLISSAGGFILETAV--RRYHSLSTYGPVLNGVGGNLAAVQA
HP SRISTYLHMWSAPGVLP LQ--MKKFWPNPCSTFCTSEINSMSARVLLLLLVVPGHLIF-FY
   **..**..* . . ***** . ....* . . ..* ..* ..*.....*****. * *
CE SRLSTYFHKAGTVGVLPNEWTVSRF-TSVQRAFFSKEWDSRSARVLLLLLVVPGHICFNFL
HP I-IYLVEGQSVINSQ--TFVVLYLLAGLIQVTILLYLAEVMVRLTWHQALDPDNHCIPYL
25  * .. .... . . . . * . **..*...*****.***... ..* * * . ***** ****
CE IQLFTLTSKNNVTPHGPLFTSLYMIAAIIQVVILLFVCQLLVALLWKWKIDPDNSVIPYL
HP TGLGDL LGTGLLALCFFTDWLLKSKAELGGISELASGPP
   *.*****. . *. *
CE TALGDL LGTGLLFIVFLTTDHFDPKELTSS

30

```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. AA334000) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

5

<HP10530> (SEQ ID Nos. 96, 106, and 116)

Determination of the whole base sequence of the cDNA insert of clone HP10530 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure
10 consisting of a 80-bp 5'-untranslated region, a 1182-bp ORF, and a 95-bp 3'-untranslated region. The ORF codes for a protein consisting of 393 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 36 depicts the hydrophobicity/hydrophilicity profile,
15 obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 46 kDa that was somewhat larger than the molecular weight of 44,912 predicted from the ORF. In this case, the addition of a microsome led to the formation
20 of a product of 45.5 kDa from which the secretory signal is considered to have been cleaved. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from lysine at position 23. When expressed in
25 COS7 cells, an expression product of about 43 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the
30 protein was similar to the Arabidopsis thaliana hypothetical protein IG002N01 (GenBank Accession No. AF007269). Table 25 shows the comparison between amino acid sequences of the

human protein of the present invention (HP) and the A.
thaliana hypothetical protein IG002N01 (AT). Therein, the
marks of -, *, and . represent a gap, an amino acid residue
identical with that of the protein of the present invention,
5 and an amino acid residue similar to that of the protein of
the present invention, respectively. The both proteins
shared a homology of 27.0% in the N-terminal region of 355
amino acid residues.

Table 25

HP	MRTLFLNLLWL
5	AT MELTSFQKSPSSNDVVSFSVSLVRNSMARRRRSSAAESLKRRNDGYESLCQVVQQDSDRR HP ALACSPVHTTLSKSDAKKAASKTLEKSQFSDKPVQDRGLVVTDLKAESVVLEHRSYCSA*.* **.. **.. ..
10	AT LITIFVIFVIVIPAVSIAVYKVKFADRVIQTESSIRQKGIVKTDINFQEILTEHSK--AS HP KARDRHFAGDVLGYVTPWNSHGYDVTKVFGSKFTQISPVLQ-LKRRGREMF EVTGLHNDV**.. **.*.*. ..* .. *.... . . **.*.*..... . **.*. AT ENSTRHYDYPVLAYITP--CQGSGL--VLEGR-HNADKGWIQELRSRGNALSASKGLPKL HP DQGWMRAVRKHAKGLHIVPRLLFEDWTYDDFRNVLDSEDEIEELSKTVVQVAKNQHFDDGF * * . ** ..*.* *.*
15	AT ---YNSCIFHALKRMNFFTLELVNFNTYLVIMFALNS-REMEYNGIVLESWSRWAAYGVL HP VVEVWNQLLSQKRVGLIHMLTHLAEALHQARLLALLVIPPAITPGTDQLGMFTHKEFEQL * . * * . *.....* AT HDPDLRKMALKFVKQLGDALHSTSSPRNNQOHMQFMYVVGPPRSEKLQMYDFGPEDLQFL HP APVLDGFSMLTYDYSTAHPGPNAPLSWVRACVQ-VLDPKSK---WRSKILLGLNIFYGM .*****.*.....*****.*. . . *..... .*****.*****
20	AT KDSVDGFSMLTYDFSNPQNP GP NAPVKWIDLTCLKLLGSSNNIDSNIARKVLLGINIFYGN HP DYATSKDAREPVVGARYIQTLKDHPRPMVWDSQASEHFF EYKKSRSRGRHVVFYPTLKSLLQ *...* ..*.....* *..*.....* ..*.....* *.....*.....*.....* AT DFVISGGGGGAITGRDYLLALLQKHKPTFRWDKESGEHLFMYRDDKNIKHAVFYPTLMSIL HP VRLELARELGVGVSIEWELGQGLDYFYDLL
25	.*** ** *.*.....*.*. ... AT LRLENARLWGIGISIEWEIGQDKGHFGKYAEASLEASSIFSGHTFDMQFRTNPRQLSRNGS

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA302913) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the

protein of the present invention.

<HP10541> (SEQ ID Nos. 97, 107, and 117)

Determination of the whole base sequence of the cDNA
5 insert of clone HP10541 obtained from cDNA library of human
stomach cancer revealed the structure consisting of a 7-bp
5'-untranslated region, a 591-bp ORF, and a 113-bp 3'-
untranslated region. The ORF codes for a protein consisting
of 196 amino acid residues and there existed a putative
10 secretory signal at the N-terminus. Figure 37 depicts the
hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of 23 kDa that was somewhat larger than the molecular weight
15 of 21,553 predicted from the ORF. In this case, the addition
of a microsome led to the formation of a product of 20 kDa
from which the secretory signal is considered to have been
cleaved and a product of 23 kDa which is considered to have
a sugar chain being attached. Application of the (-3,-1)
20 rule, a method for predicting the cleavage site of the
secretory signal sequence, allows to expect that the mature
protein starts from glycine at position 41. In addition,
there exists in the amino acid sequence of this protein one
site at which N-glycosylation may occur (Asn-Leu-Thr at
25 position 185).

The search of the protein data base using the amino
acid sequence of the present protein revealed that the
protein was similar to the human zymogen membrane protein
(GenBank Accession No. AF056492). Table 26 shows the
30 comparison between amino acid sequences of the human protein
of the present invention (HP) and the human zymogen membrane
protein (ZM). Therein, the marks of -, *, and . represent a

gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 37.6% in the C-terminal region of 133 amino acid residues.

Table 26

10	HP MWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFS-TTEDYD	**.***** ** *
	ZM MLTVALLALLCASASGNAIQARSSSYSGEYGS GGGKRF SHSGNQLD	
	HP HEITGLRVS VGLLLVKSVQVKLGDSWDVKLGALGGNTQEVTLQPGEYITKVFAVQAF LR	
		.***. * . * . . * . * . . * . * . . . * . . . *
	ZM GPITALRVRVNTYYIVGLQVRYGKVWSDYVGG R NGDLEEIFLHPGESVIQVSGKYK WYLK	
15	HP GMVMYTSKDRYFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIK SIGFEWN-YPLEEP	
		. * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
	ZM KLVFVTDKGRYLSFGKDSGTSFNAVPLHPNTVLRFISGRSGSL-IDAIGLHWDVYPTSCS	
	HP TTEPPVNLTYSANSPVGR	
20	ZM RC	

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA340605) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

30

<HP10550> (SEQ ID Nos. 98, 108, and 118)

Determination of the whole base sequence of the cDNA

insert of clone HP10550 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 241-bp 5'-untranslated region, a 324-bp ORF, and a 86-bp 3'-untranslated region. The ORF codes for a protein consisting of 107 amino acid residues and there existed one putative transmembrane domain. Figure 38 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA348310) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10590> (SEQ ID Nos. 99, 109, and 119)

Determination of the whole base sequence of the cDNA insert of clone HP10590 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 77-bp 5'-untranslated region, a 1053-bp ORF, and a 180-bp 3'-untranslated region. The ORF codes for a protein consisting of 350 amino acid residues and there existed one putative transmembrane domain. Figure 39 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 40 kDa that was almost identical with the molecular weight of 39,285 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of

43 kDa which is considered to have a sugar chain being attached. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Asn-Ser at position 144 and Asn-Leu-Thr at position 328).

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA461346) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10591> (SEQ ID Nos. 100, 110, and 120)

Determination of the whole base sequence of the cDNA insert of clone HP10591 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 232-bp 5'-untranslated region, a 324-bp ORF, and a 844-bp 3'-untranslated region. The ORF codes for a protein consisting of 107 amino acid residues and there existed one putative transmembrane domain. Figure 40 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,328 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H09424) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein

of the present invention.

<HP01462> (SEQ ID Nos. 121, 131, and 141)

Determination of the whole base sequence of the cDNA
5 insert of clone HP01462 obtained from cDNA library of human
fibrosarcoma cell line HT-1080 revealed the structure
consisting of a 121-bp 5'-untranslated region, a 1452-bp ORF,
and a 477-bp 3'-untranslated region. The ORF codes for a
protein consisting of 483 amino acid residues and there
10 existed a putative secretory signal at the N-terminus.
Figure 41 depicts the hydrophobicity/hydrophilicity profile,
obtained by the Kyte-Doolittle method, of the present
protein. In vitro translation resulted in formation of a
translation product of 72 kDa that was larger than the
15 molecular weight of 55,838 predicted from the ORF.
Application of the (-3,-1) rule, a method for predicting the
cleavage site of the secretory signal sequence, allows to
expect that the mature protein starts from lysine at
position 21.

20 The search of the protein data base using the amino
acid sequence of the present protein revealed that the
protein was similar to the *Caenorhabditis elegans*
hypothetical protein ZK1058.4 (EMBL Accession No. Z35604).
Table 27 shows the comparison between amino acid sequences
25 of the human protein of the present invention (HP) and the *C.*
elegans hypothetical protein ZK1058.4 (CE). Therein, the
marks of -, *, and . represent a gap, an amino acid residue
identical with that of the protein of the present invention,
and an amino acid residue similar to that of the protein of
30 the present invention, respectively. The both proteins
shared a homology of 35.6% in the entire region.

[illegible]

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. AA307793) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

5

<HP02485> (SEQ ID Nos. 122, 132, and 142)

Determination of the whole base sequence of the cDNA insert of clone HP02485 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 69-bp
10 5'-untranslated region, a 1005-bp ORF, and a 1672-bp 3'-untranslated region. The ORF codes for a protein consisting of 334 amino acid residues and there existed one putative transmembrane domain. Figure 42 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-
15 Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36 kDa that was almost identical with the molecular weight of 38,171 predicted from the ORF. When expressed in COS7 cells, an expression product of about 23 kDa was
20 observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein W01A11.2 (GenBank Accession No. U64852).
25 Table 28 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein W01A11.2 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of
30 the present invention, respectively. The both proteins shared a homology of 45.5% in the entire region.

insert of clone HP02798 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 31-bp 5'-untranslated region, a 804-bp ORF, and a 301-bp 3'-untranslated region. The ORF codes for a
5 protein consisting of 267 amino acid residues and there existed four putative transmembrane domains. Figure 43 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation
10 product of 29 kDa that was almost identical with the molecular weight of 30,778 predicted from the ORF. When expressed in COS7 cells, an expression product of about 26 kDa was observed in the membrane fraction.

The search of the protein data base using the amino
15 acid sequence of the present protein revealed that the protein was similar to the human DHHC-containing cysteine-rich protein (GenBank Accession No. U90653). Table 29 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human DHHC-containing cysteine-rich protein (DH). Therein, the marks of
20 -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a
25 homology of 35.0% in the intermediate region of 100 amino acid residues. The positions of seven cysteines were conserved between the two proteins. The protein of the present invention also had the DHHC (Asp-His-His-Cys) sequence.

Table 29

	HP	MAPWALLSPGVLVRTGHTVLTWGI
5	DH MYKMNICNKPSNKTAPESVWTAPAQPSGSPPELQGQSRNRNGWSWPPHPLQIVAWLLYL	
	HP TLVFLFLHDTLRLQWEEQGELLPLTFLLLVLGSLLLYLAVSLMDPGYVNVQPQP-QEELK	
		* * * * *
	DH FFAVIGFGILVPLLPHHWVPAGYACMGAIFAGHLVVHLTAVSIDPADDNVRDKSYAGPLP	
	HP EEQTAMVPPAIPLRRCRYCLVLQPLRARHCRECRRCVRRYDHHCPWMENCVGERNHPLFV	
10 * . * . * . * * * * *	
	DH IFNRSQHAHVIEDLHCNLCNVDVSARSKHCSACNKCVCGFDDHCKWLNNCVGERNYRLFL	
	HP VYLALQLVLLWGLYLAWSGLRFFQPWGLWLRSSGLLFATFLLLSLFSIVASLLLVSHLY	
	. * . * . *	
	DH HSVASALLGVLLLVLGGHICLRGVLCQPHASAHQPTL	
15		

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. D79050) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

25 <HP10041> (SEQ ID Nos. 124, 134, and 144)

Determination of the whole base sequence of the cDNA insert of clone HP10041 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 12-bp 5'-untranslated region, a 321-bp ORF, and a 286-bp 3'-untranslated region. The ORF codes for a protein consisting of 106 amino acid residues and there existed one putative transmembrane domain. Figure 44 depicts

the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 12,060 predicted from the ORF. When expressed in COS7 cells, an expression product of about 13 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein K10B2.4 (GenBank Accession No. U28730). Table 30 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein K10B2.4 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 62.1% in the entire region.

Table 30

HP	MSTNNMSDPRRPKNVLRYP---PPSECNPALDDPTPDYMNLLGMIFSMCGLMLKLKWCA
	.****.*...****
CE	MQQNGDPRRTNRIVRYKPLDSTANQQQAISEDPLPEYMNVLGMIFSMCGLMIRMKWCS
HP	WVAVYCSFISFANSRSEDTKQMMSSFMLSISAVVMSYLQNPQPMTPPW
	.. ** *****.*.*.*.*.*****.***** *..***
CE	WLALVCSCISFANTRTSDDAKQIVSSFMLSISAVVMSYLQNPSPPIPPWVTLQOS

Furthermore, the search of the GenBank using the base

sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H20098) in ESTs, but, since they are partial sequences, it can not be judged whether or not any
5 of these sequences codes for the same protein as the protein of the present invention.

<HP10246> (SEQ ID Nos. 125, 135, and 145)

Determination of the whole base sequence of the cDNA
10 insert of clone HP10246 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 110-bp 5'-untranslated region, a 675-bp ORF, and a 79-bp 3'-untranslated region. The ORF codes for a protein consisting of 224 amino acid residues and there
15 existed five putative transmembrane domains. Figure 45 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 23 kDa that was somewhat smaller than the
20 molecular weight of 25,244 predicted from the ORF. When expressed in COS7 cells, an expression product of about 21 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the
25 protein was similar to the human putative seven transmembrane domain protein (GenBank Accession No. Y18007). Table 31 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human putative seven transmembrane domain protein (TM).
30 Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that

of the protein of the present invention, respectively. The both proteins shared a homology of 93.3% in the entire region.

5

Table 31

```

HP MTLFHFNGCFALAYFPYFITYKCSGLSEYNAFWKCVQAGVTYLFVQLCKMLFLATFFPTW
*****.*****
TM MTLFHFNGCFALAYFPYFITYKCTDLSEYNAFWKCVQAGVTYLFVQLCKMLFLATFFPTW
10 HP EGGIYDFIGEFMKASVDVADLIGLNLVMSRNAGKGEYKIMVAALGWATAELIMSRCIPLW
*****
TM EGGIYDFIGEFMKASVDVADLIGLNLVMSRNAGKGEYKIMVAALGWATAELIMSRCIPLW
HP VGARGIEFDWKYIQMSIDSNISLVHYIVASAQVWMITRYDLYHTFRPAVLLLMFLSVYKA
*****.*****.****
15 TM VGARGIEFDWKYIQMSIDSNISLGPYIVASAQVWMITRYDLYHTFRPAVLLLMFLRVYKA
HP FVMETFVHLC SLG SWAALLARAVVTGLLALSTLALYVAVVNVHS
*****.*.*.***.....*****
TM FVMETFVHLC SLG SWAVLMAGVVVKGLLVIRNLAMYVAVVNVHS

```

20

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA453931) in ESTs, but, since they

25 are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

30

<HP10392> (SEQ ID Nos. 126, 136, and 146)

Determination of the whole base sequence of the cDNA insert of clone HP10392 obtained from cDNA library of human osteosarcoma cell line U-2 OS revealed the structure

consisting of a 24-bp 5'-untranslated region, a 777-bp ORF, and a 726-bp 3'-untranslated region. The ORF codes for a protein consisting of 258 amino acid residues and there existed a putative secretory signal at the N-terminus.

5 Figure 46 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 34 kDa that was somewhat larger than the molecular weight of 29,623 predicted from the ORF.
10 Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 49.

Furthermore, the search of the GenBank using the base
15 sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H15999) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein
20 of the present invention. In addition, partial identity with the hypothetical protein KIAA0384 (Accession No. AB002382) was observed, although the hypothetical protein had a different ORF.

25 <HP10489> (SEQ ID Nos. 127, 137, and 147)

Determination of the whole base sequence of the cDNA insert of clone HP10489 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 137-bp 5'-untranslated region, a 333-bp ORF, and a 189-bp 3'-
30 untranslated region. The ORF codes for a protein consisting of 110 amino acid residues and there existed two putative transmembrane domains. Figure 47 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 19 kDa that was somewhat larger than the molecular weight of 12,010 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA262162) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10519> (SEQ ID Nos. 128, 138, and 148)

Determination of the whole base sequence of the cDNA insert of clone HP10519 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 67-bp 5'-untranslated region, a 276-bp ORF, and a 367-bp 3'-untranslated region. The ORF codes for a protein consisting of 91 amino acid residues and there existed one putative transmembrane domain. Figure 48 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was almost identical with the molecular weight of 10,275 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W16639) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein

of the present invention.

<HP10531> (SEQ ID Nos. 129, 139, and 149)

Determination of the whole base sequence of the cDNA
5 insert of clone HP10531 obtained from cDNA library of human
osteosarcoma cell line Saos-2 revealed the structure
consisting of a 55-bp 5'-untranslated region, a 1035-bp ORF,
and a 1092-bp 3'-untranslated region. The ORF codes for a
protein consisting of 344 amino acid residues and there
10 existed five putative transmembrane domains. Figure 49
depicts the hydrophobicity/hydrophilicity profile, obtained
by the Kyte-Doolittle method, of the present protein. In
vitro translation resulted in formation of a translation
product of high molecular weight.

15 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. R50695) in ESTs, but, since they are
partial sequences, it can not be judged whether or not any
20 of these sequences codes for the same protein as the protein
of the present invention.

<HP10574> (SEQ ID Nos. 130, 140, and 150)

Determination of the whole base sequence of the cDNA
25 insert of clone HP10574 obtained from cDNA library of human
stomach cancer revealed the structure consisting of a 210-bp
5'-untranslated region, a 1287-bp ORF, and a 1276-bp 3'-
untranslated region. The ORF codes for a protein consisting
of 428 amino acid residues and there existed a putative
30 secretory signal at the N-terminus and one putative
transmembrane domain in the intermediate region. Figure 50
depicts the hydrophobicity/hydrophilicity profile, obtained

by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from serine at position 36.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Drosophila melanogaster GOLIATH protein (SWISS-PROT Accession No. Q06003). Table 32 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the D. melanogaster GOLIATH protein (DM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The intermediate region of 169 amino acids of the protein of the present invention shared a homology of 41.4% with the N-terminal region of the D. melanogaster GOLIATH protein.

The present invention provides human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic cells expressing these DNAs. All of the proteins of the present invention are secreted or exist in the cell membrane, so that they are considered to be proteins controlling the proliferation and/or the differentiation of the cells. Accordingly, the proteins of the present invention can be employed as pharmaceuticals such as carcinostatic agents which act to control the proliferation and/or the differentiation of the cells, or as antigens for preparing antibodies against these proteins. The DNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the DNAs can be utilized for large-scale expression of these proteins. Cells into which these genes are introduced to express these proteins, can be utilized for detection of the corresponding receptors and ligands, screening of novel low-molecular pharmaceuticals, and so on.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or

primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254; Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished

through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, Bioessays 14(9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA 90(16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci. USA 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour et al., 1988, Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614, 396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s). Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more

preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide, as determined by those of skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the polynucleotides.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides

capable of hybridizing under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the

5 table 33 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 33

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
A	DNA : DNA	≥50	65°C; 1×SSC -or- 42°C; 1×SSC, 50% formamide	65°C; 0.3×SSC
B	DNA : DNA	<50	T _B [*] ; 1×SSC	T _B [*] ; 1×SSC
C	DNA : RNA	≥50	67°C; 1×SSC -or- 45°C; 1×SSC, 50% formamide	67°C; 0.3×SSC
D	DNA : RNA	<50	T _D [*] ; 1×SSC	T _D [*] ; 1×SSC
E	RNA : RNA	≥50	70°C; 1×SSC -or- 50°C; 1×SSC, 50% formamide	70°C; 0.3×SSC
F	RNA : RNA	<50	T _F [*] ; 1×SSC	T _F [*] ; 1×SSC
G	DNA : DNA	≥50	65°C; 4×SSC -or- 42°C; 4×SSC, 50% formamide	65°C; 1×SSC
H	DNA : DNA	<50	T _H [*] ; 4×SSC	T _H [*] ; 4×SSC
I	DNA : RNA	≥50	67°C; 4×SSC -or- 45°C; 4×SSC, 50% formamide	67°C; 1×SSC
J	DNA : RNA	<50	T _J [*] ; 4×SSC	T _J [*] ; 4×SSC
K	RNA : RNA	≥50	70°C; 4×SSC -or- 50°C; 4×SSC, 50% formamide	67°C; 1×SSC
L	RNA : RNA	<50	T _L [*] ; 2×SSC	T _L [*] ; 2×SSC
M	DNA : DNA	≥50	50°C; 4×SSC -or- 40°C; 6×SSC, 50% formamide	50°C; 2×SSC
N	DNA : DNA	<50	T _N [*] ; 6×SSC	T _N [*] ; 6×SSC
O	DNA : RNA	≥50	55°C; 4×SSC -or- 42°C; 6×SSC, 50% formamide	55°C; 2×SSC
P	DNA : RNA	<50	T _P [*] ; 6×SSC	T _P [*] ; 6×SSC
Q	RNA : RNA	≥50	60°C; 4×SSC -or- 45°C; 6×SSC, 50% formamide	60°C; 2×SSC
R	RNA : RNA	<50	T _R [*] ; 4×SSC	T _R [*] ; 4×SSC

‡ : The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

† : SSPE (1×SSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R : The hybridization temperature for hybrids anticipated to be less than

50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, $T_m(^{\circ}\text{C}) = 2(\text{\# of A + T bases}) + 4(\text{\# of G + C bases})$. For hybrids between 18 and 49 base pairs in length, $T_m(^{\circ}\text{C}) = 81.5 + 16.6(\log_{10}[\text{Na}^+]) + 0.41(\% \text{G+C}) - (600/N)$, where N is the number of bases in the hybrid, and $[\text{Na}^+]$ is the concentration of sodium ions in the hybridization buffer ($[\text{Na}^+]$ for $1\times\text{SSC}=0.165\text{M}$).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

CLAIMS

1. A protein comprising any one of an amino acid
sequence selected from the group consisting of SEQ ID Nos. 1
5 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130.

2. An isolated DNA coding for the protein according
to Claim 1.

3. An isolated cDNA comprising any one of a base
sequence selected from the group consisting of SEQ ID Nos.
10 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140.

4. The cDNA according to Claim 3 consisting of any
one of a base sequence selected from the group consisting of
SEQ ID Nos. 21 to 30, 51 to 60, 81 to 90, 111 to 120, and
141 to 150.

15 5. An expression vector that is capable of expressing
the DNA according to any one of Claim 2 to Claim 4 by in
vitro translation or in eucaryotic cells.

6. A transformed eucaryotic cell that is capable of
expressing the DNA according to any one of Claim 2 to Claim
20 4 and of producing the protein according to Claim 1.

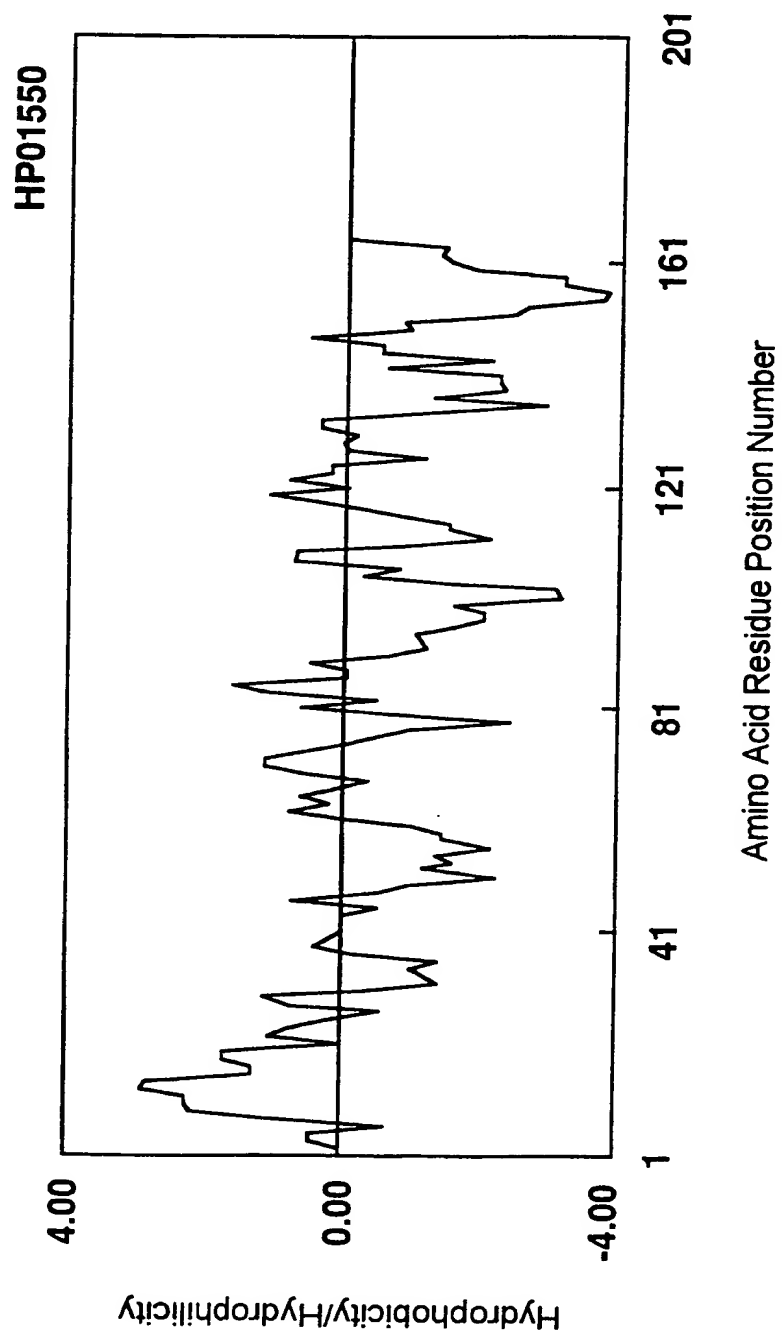


Fig. 1

2/50

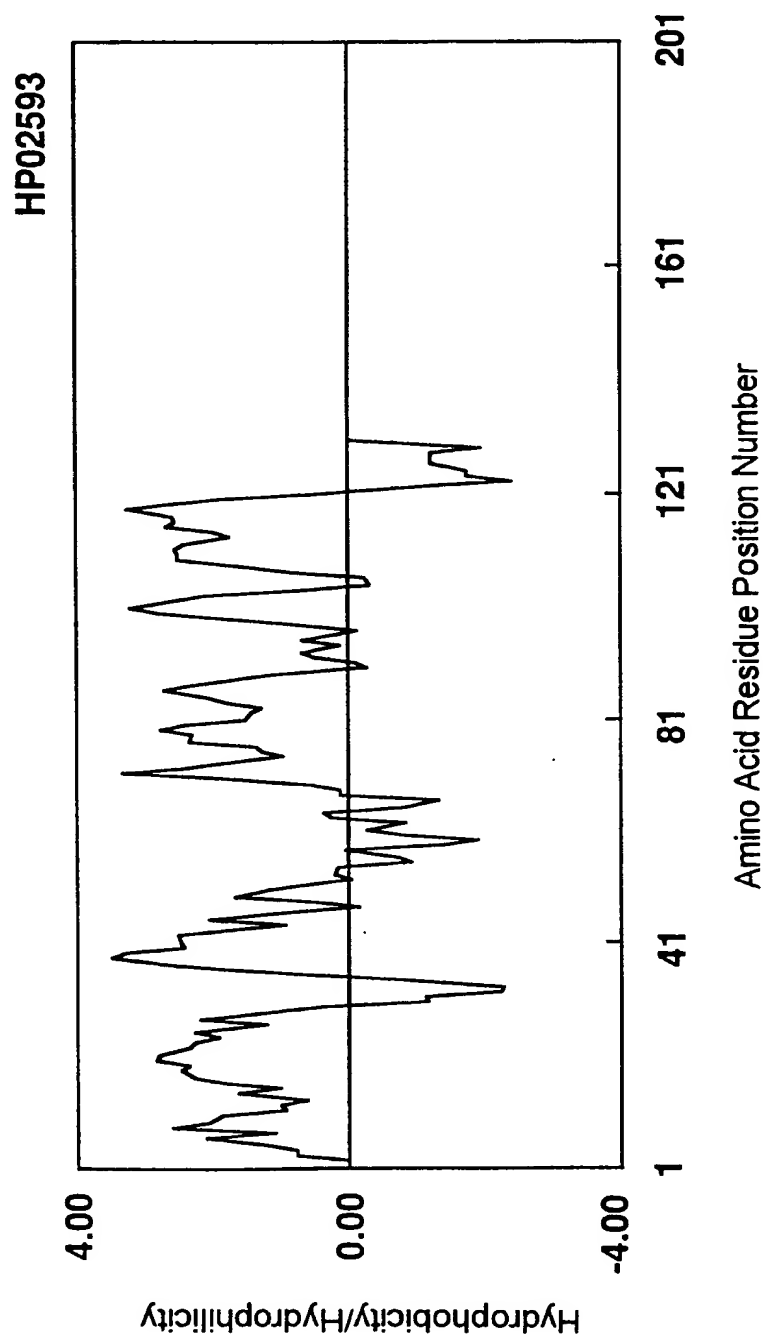


Fig. 2

3/50

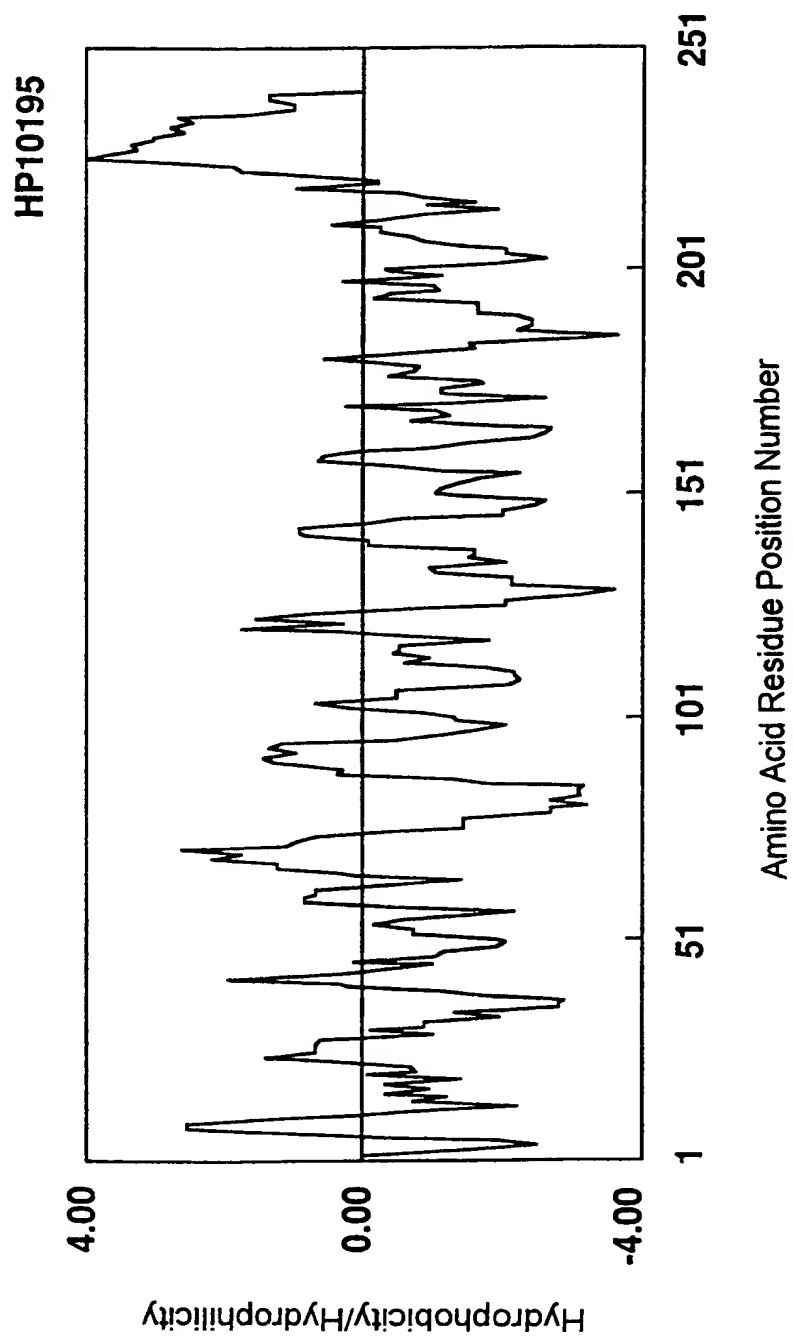


Fig. 3

4/50

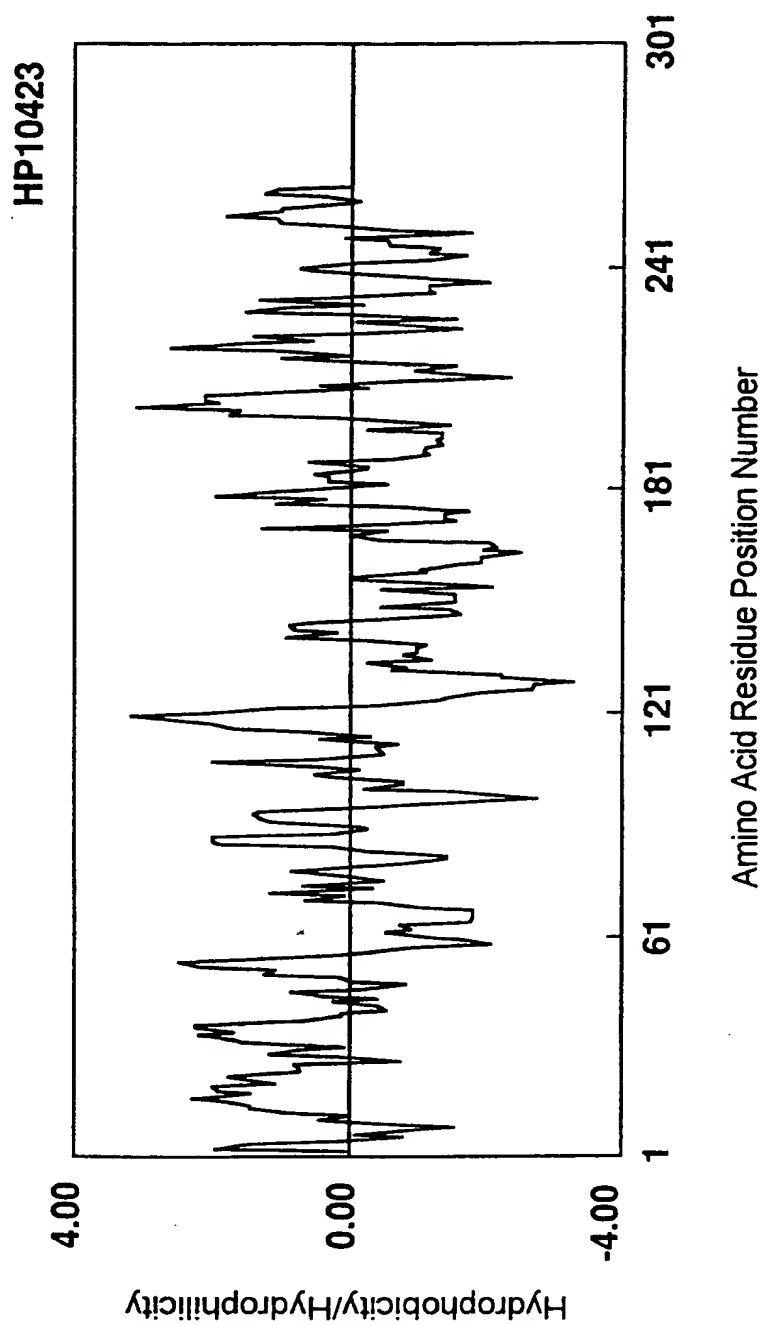


Fig. 4

5/50

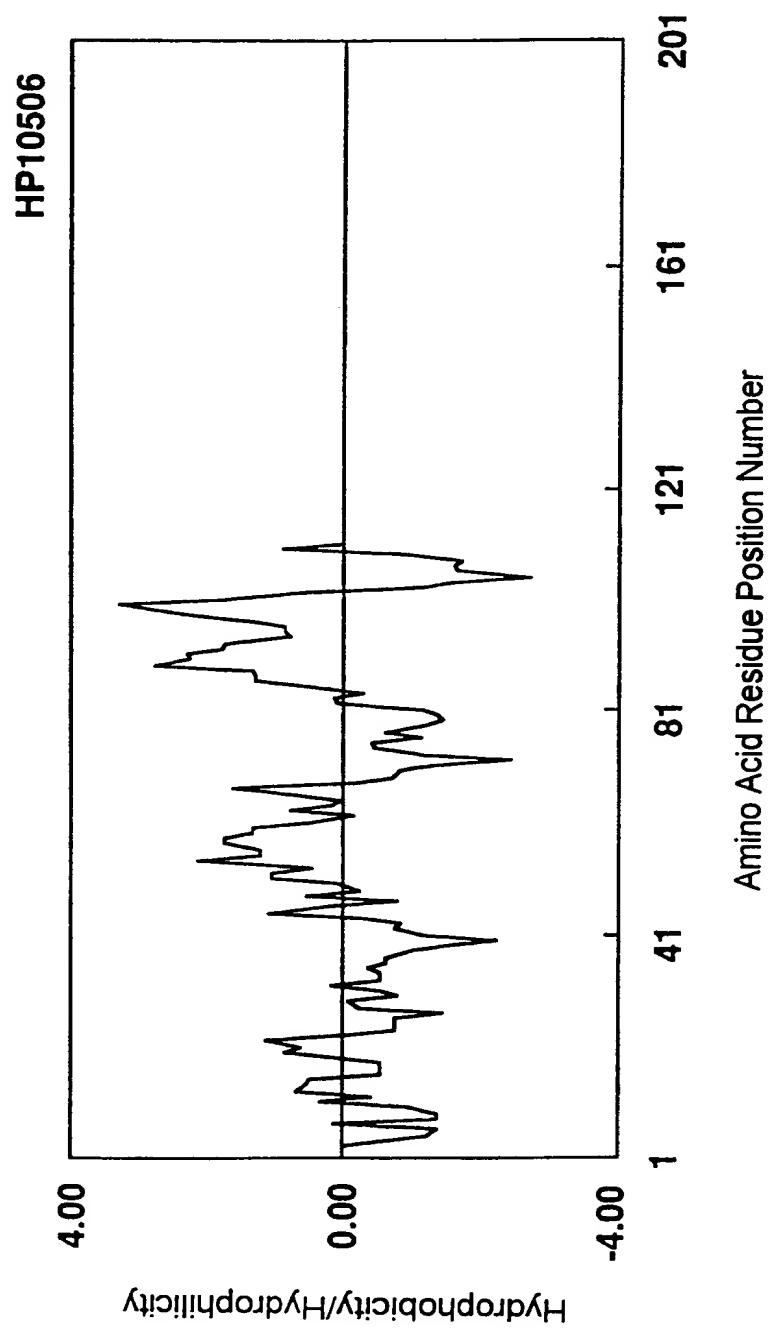


Fig. 5

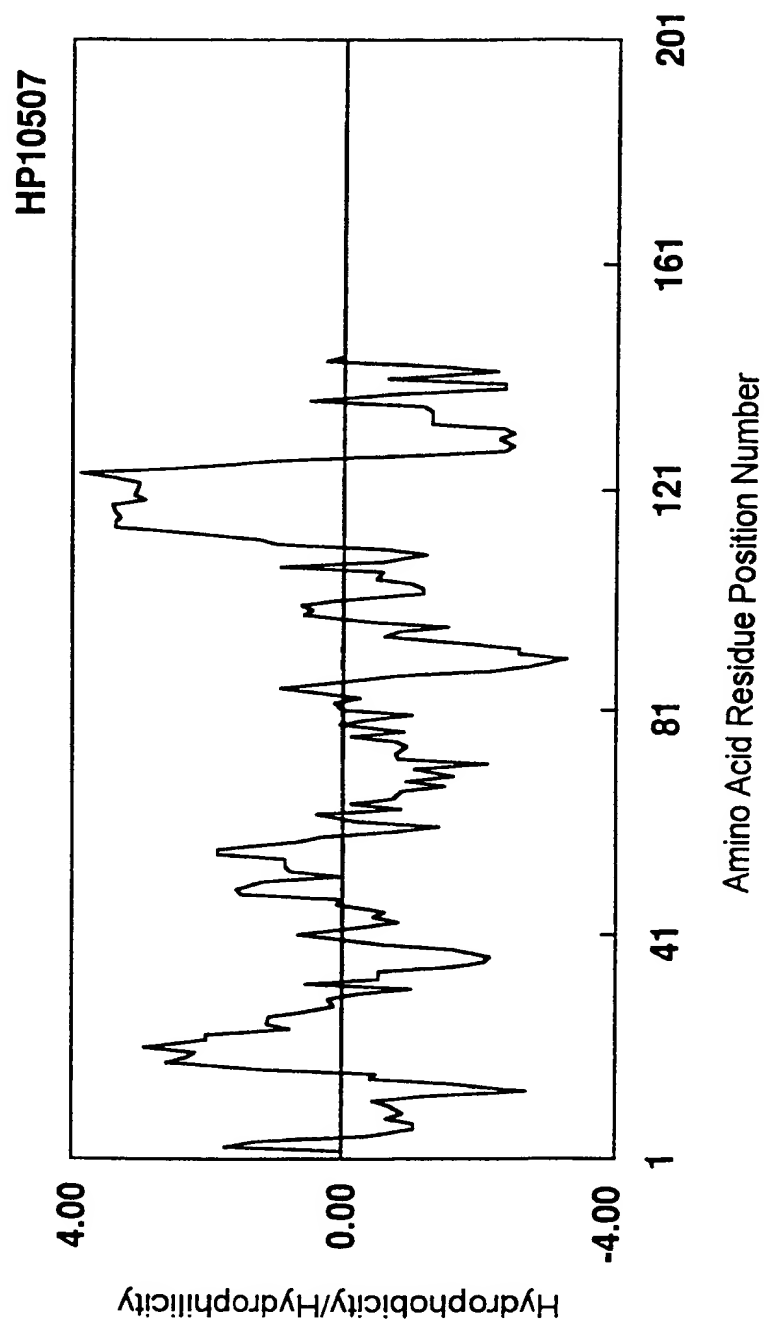


Fig. 6

7/50

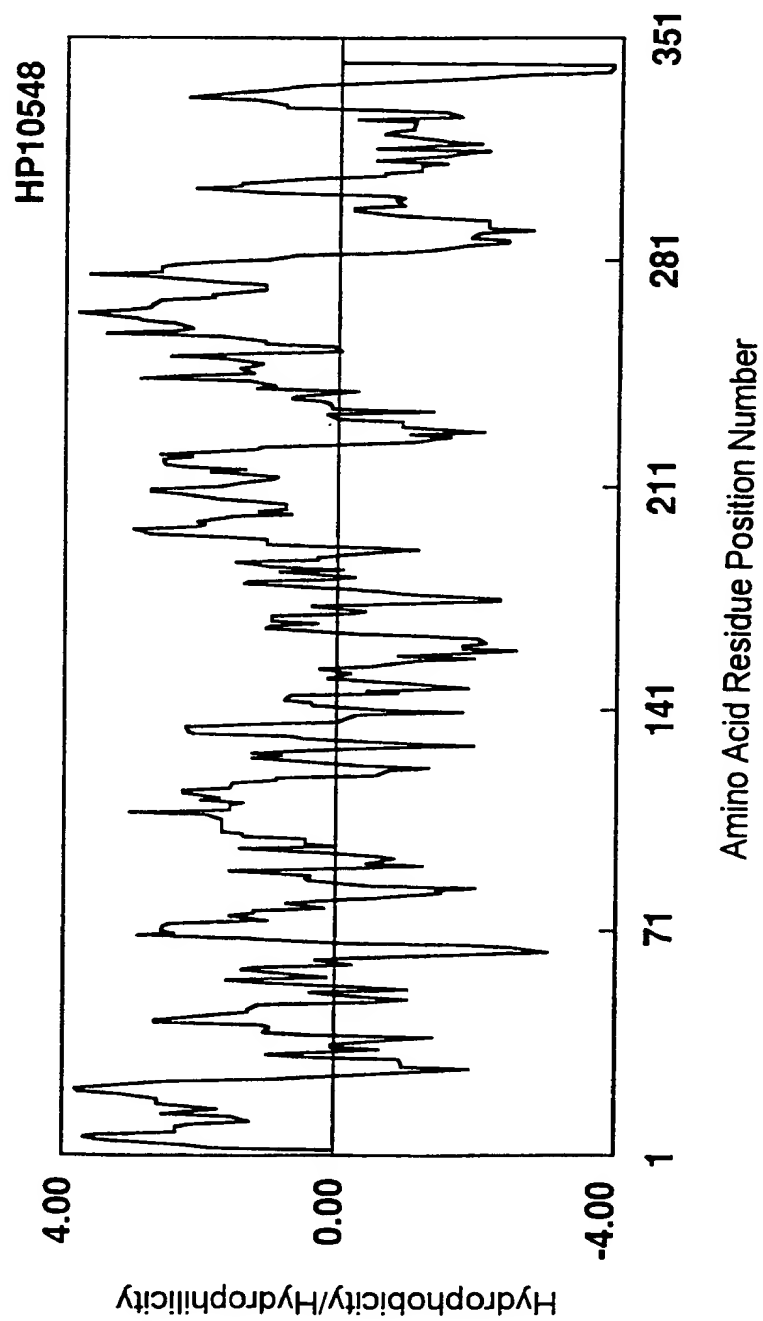


Fig. 7

8/50

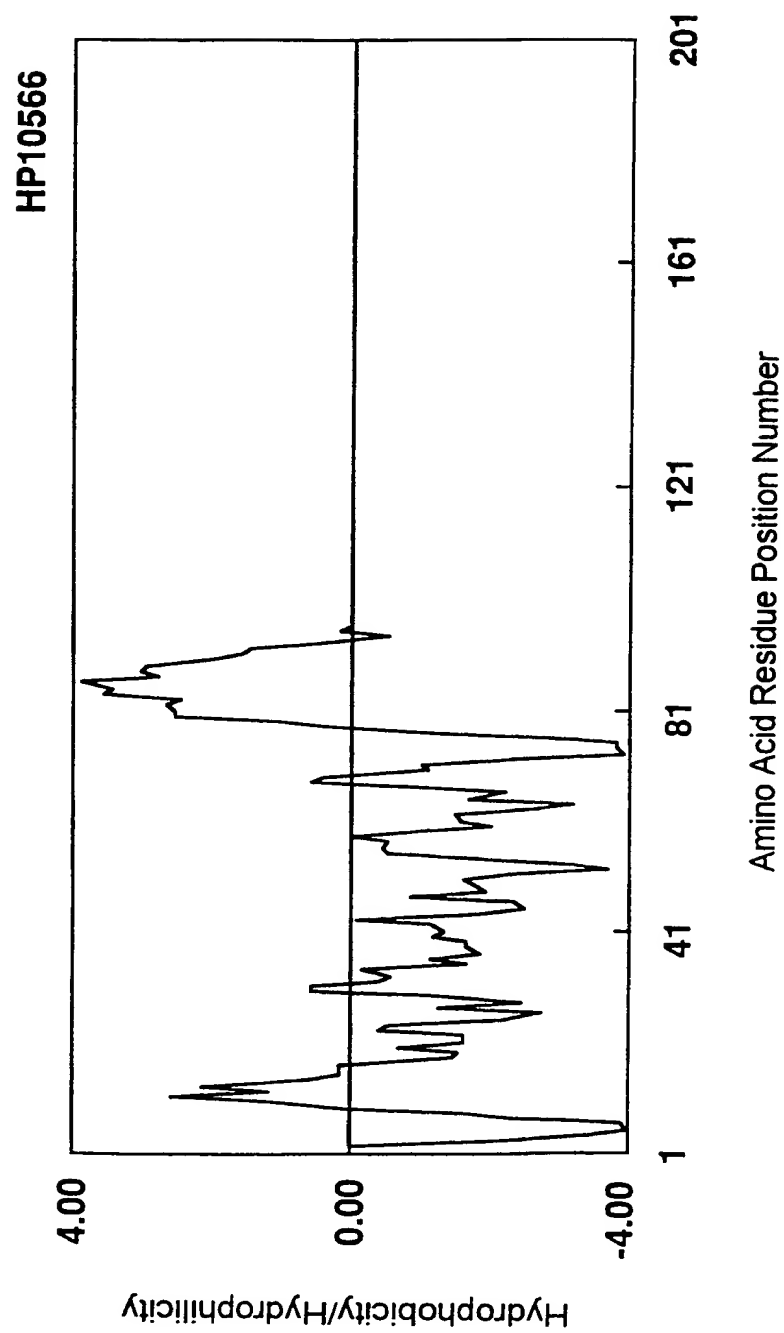


Fig. 8

9/50

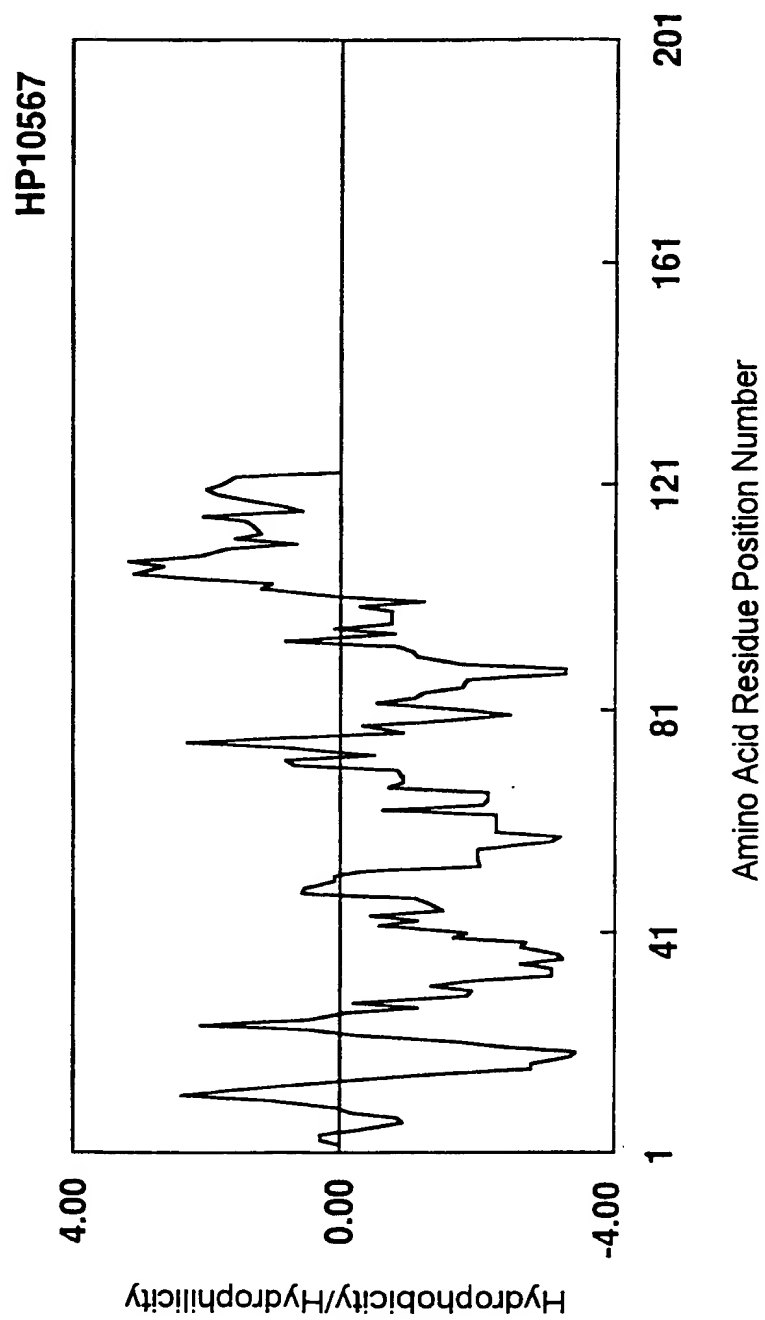


Fig. 9

10/50

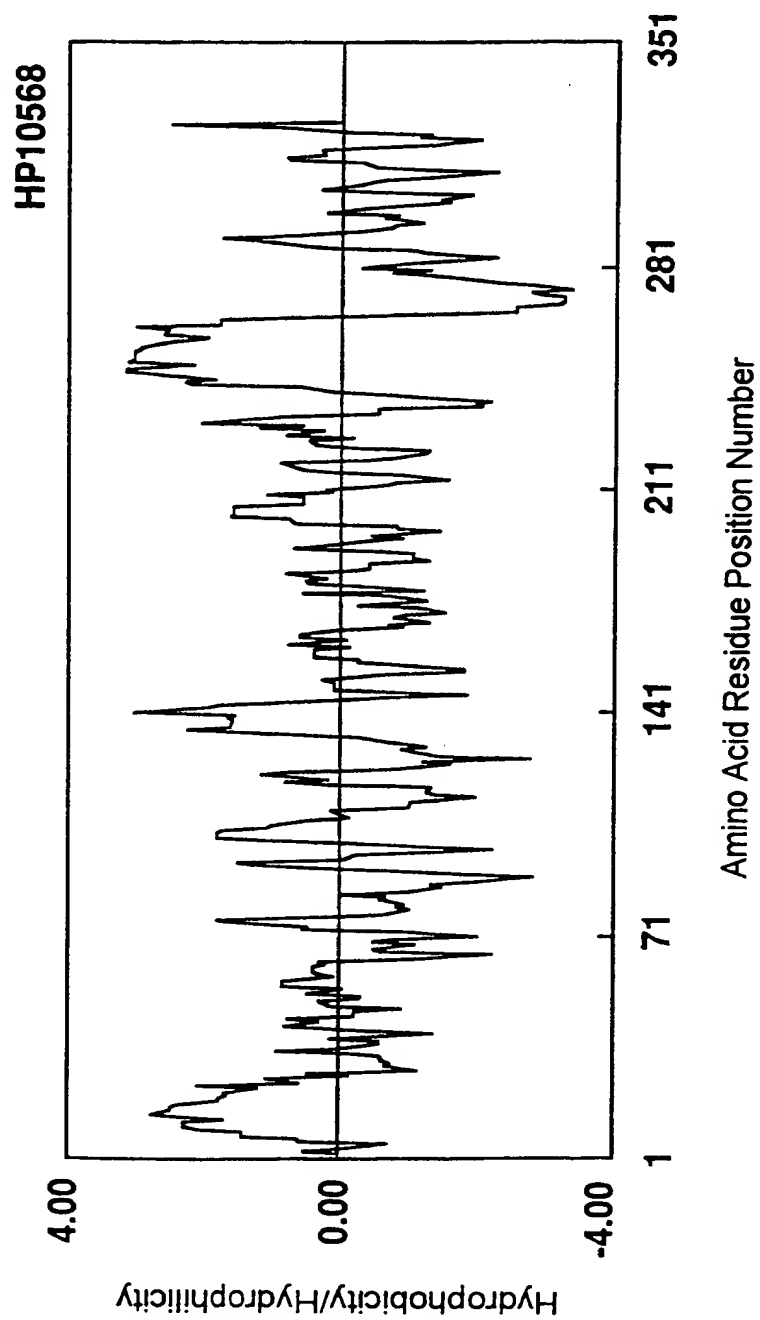


Fig. 10

11/50

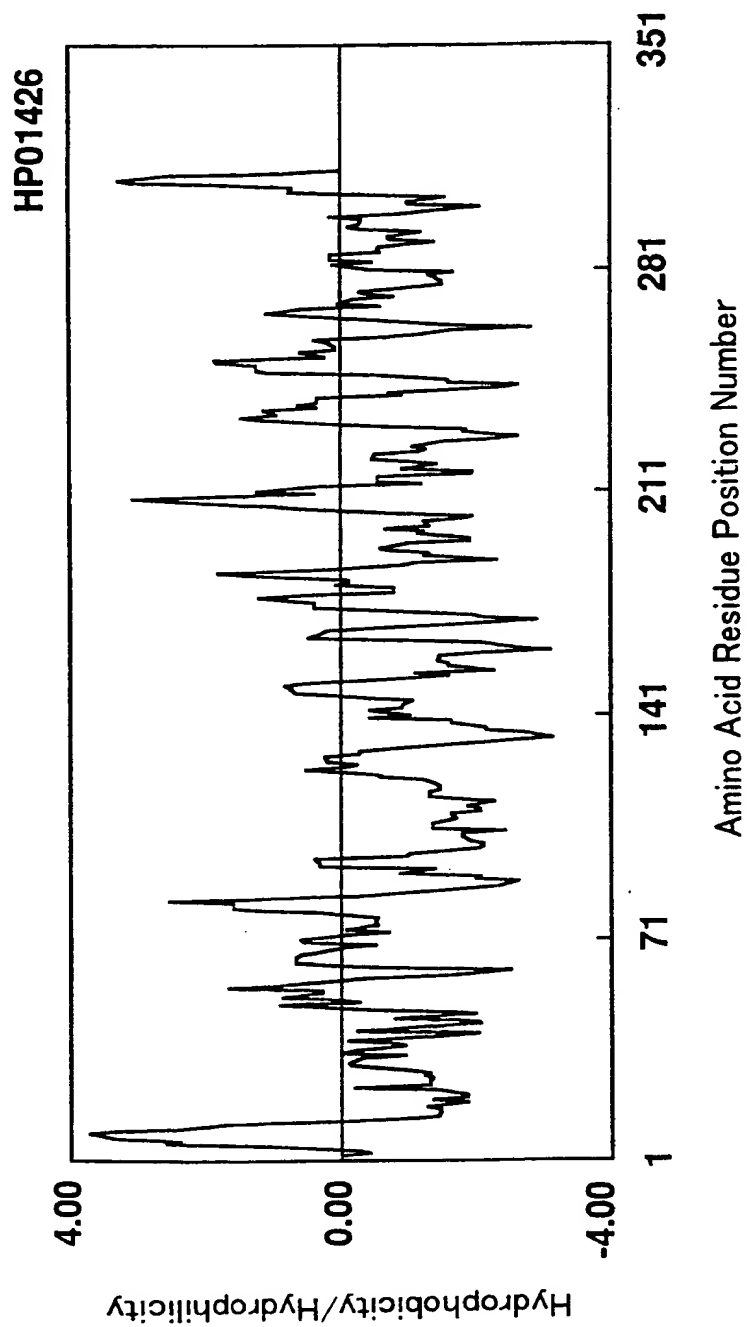


Fig. 11

12/50

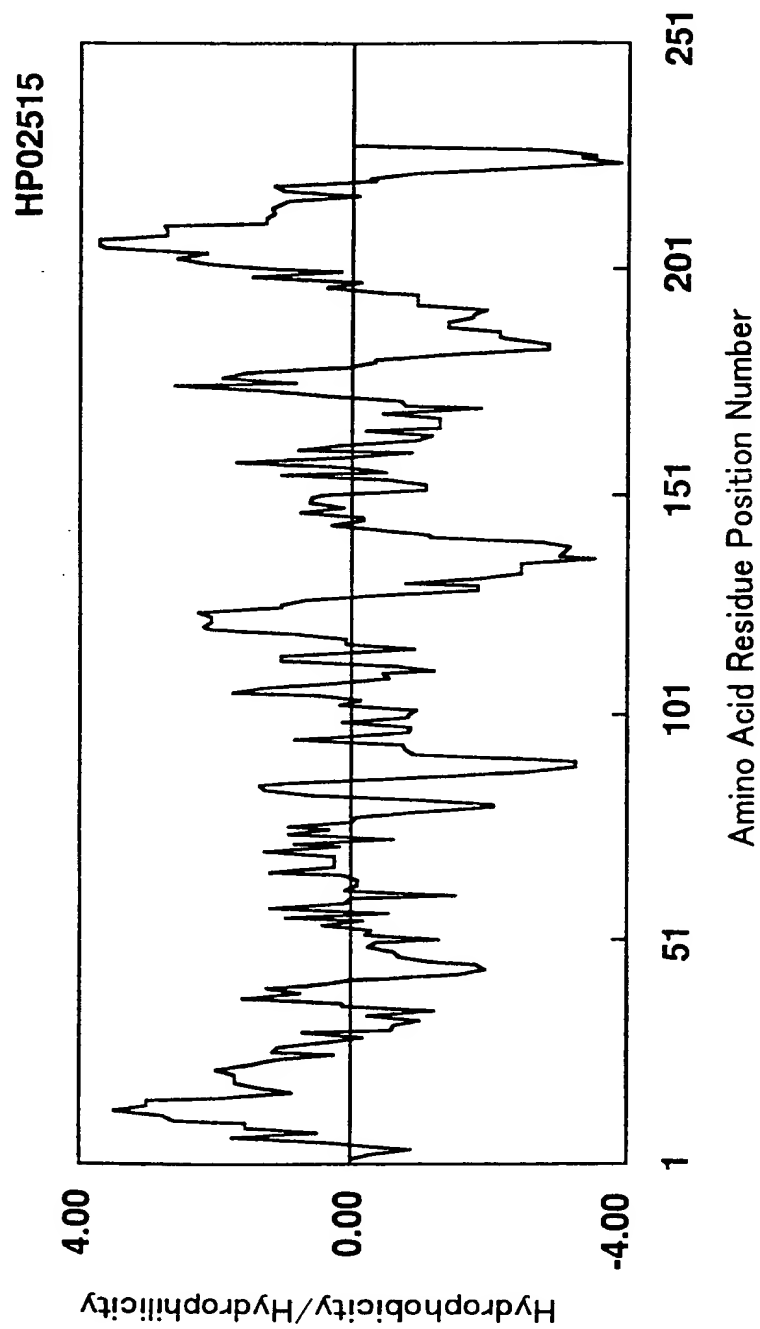


Fig.12

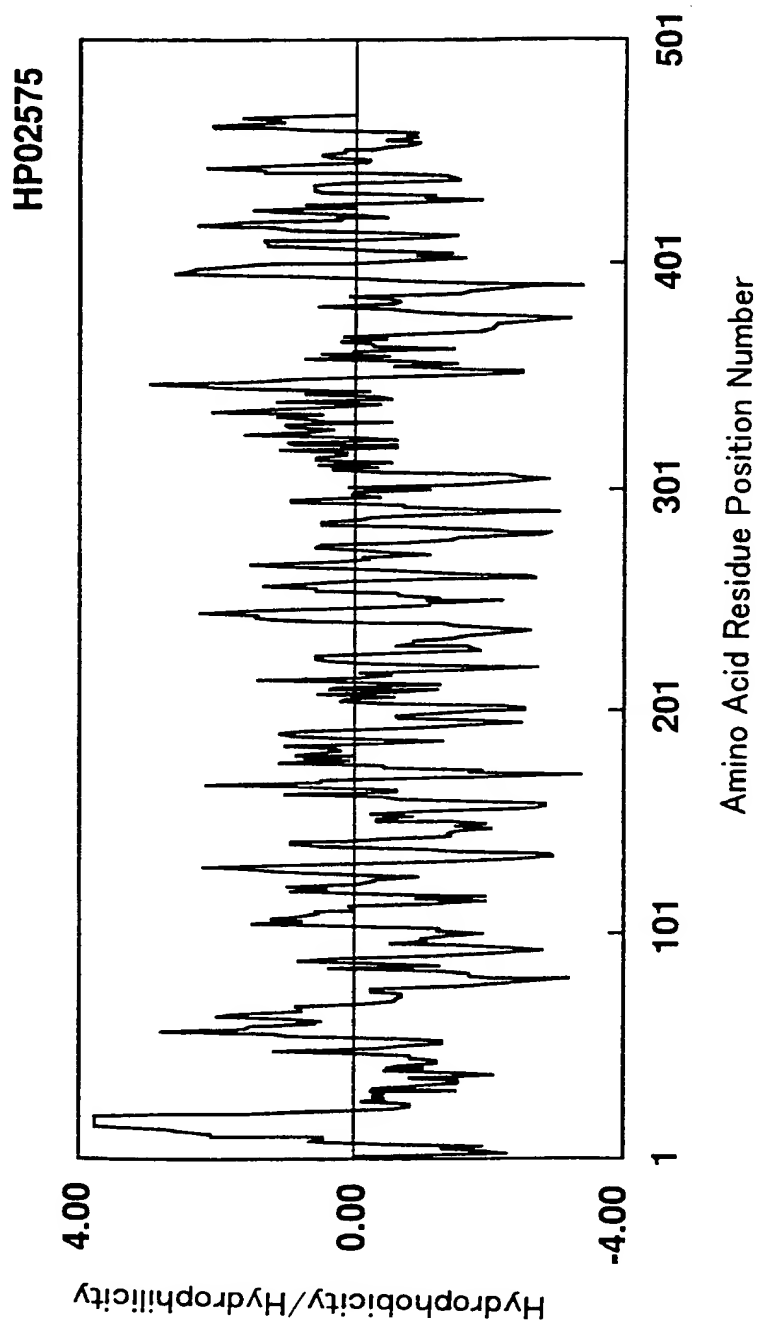


Fig. 13

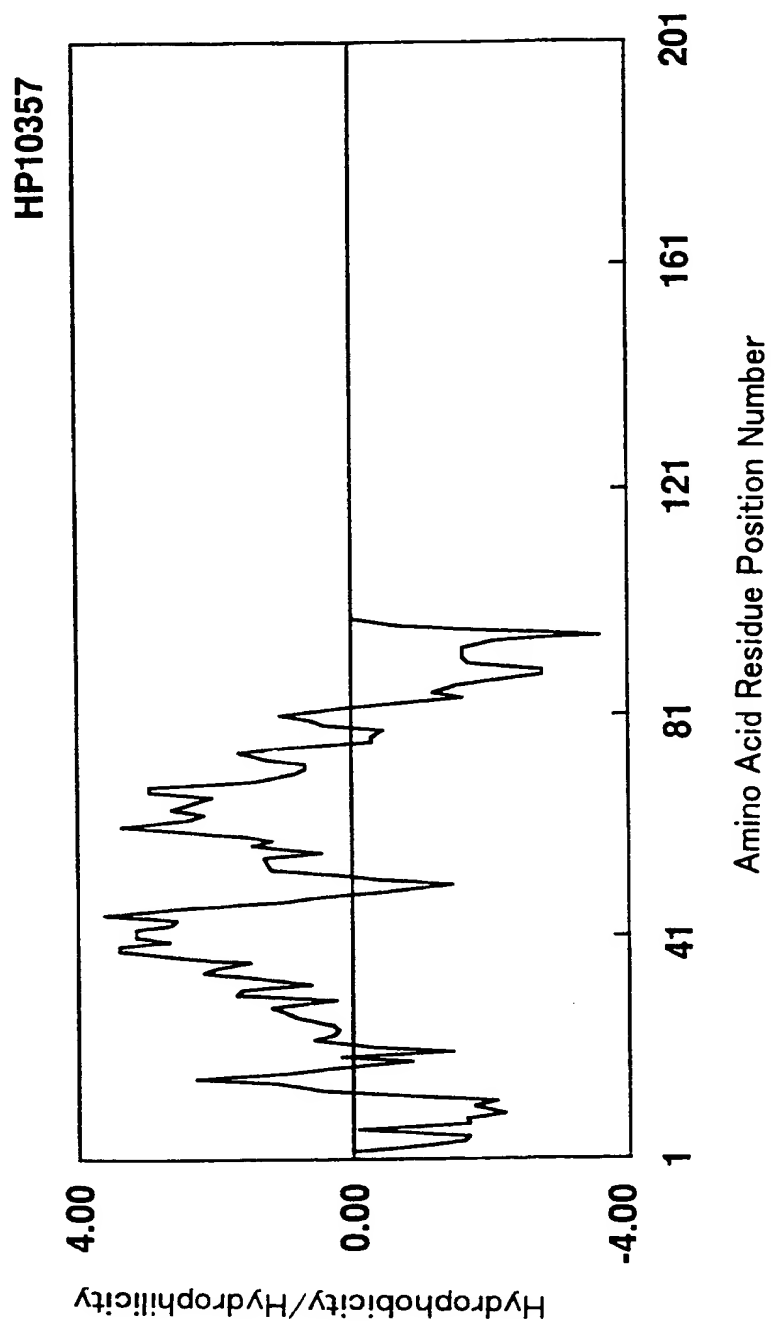


Fig. 14

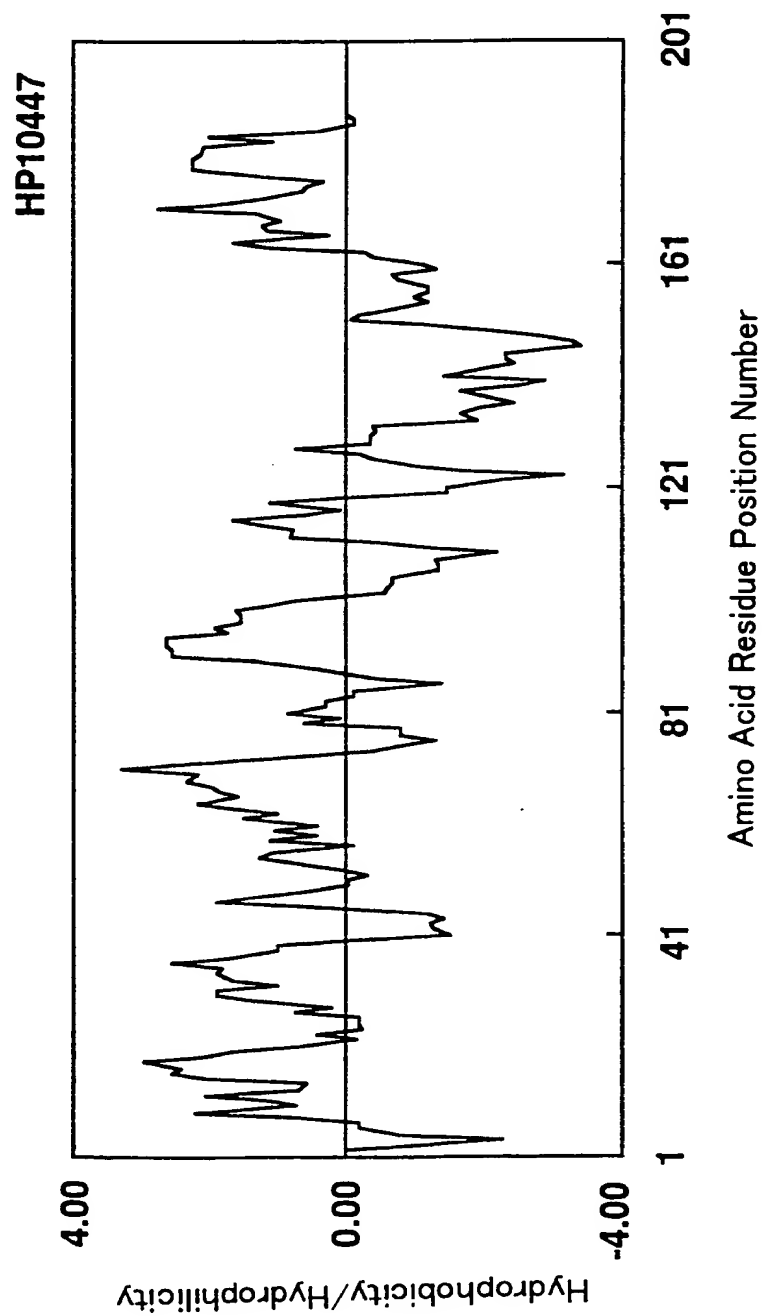


Fig. 15

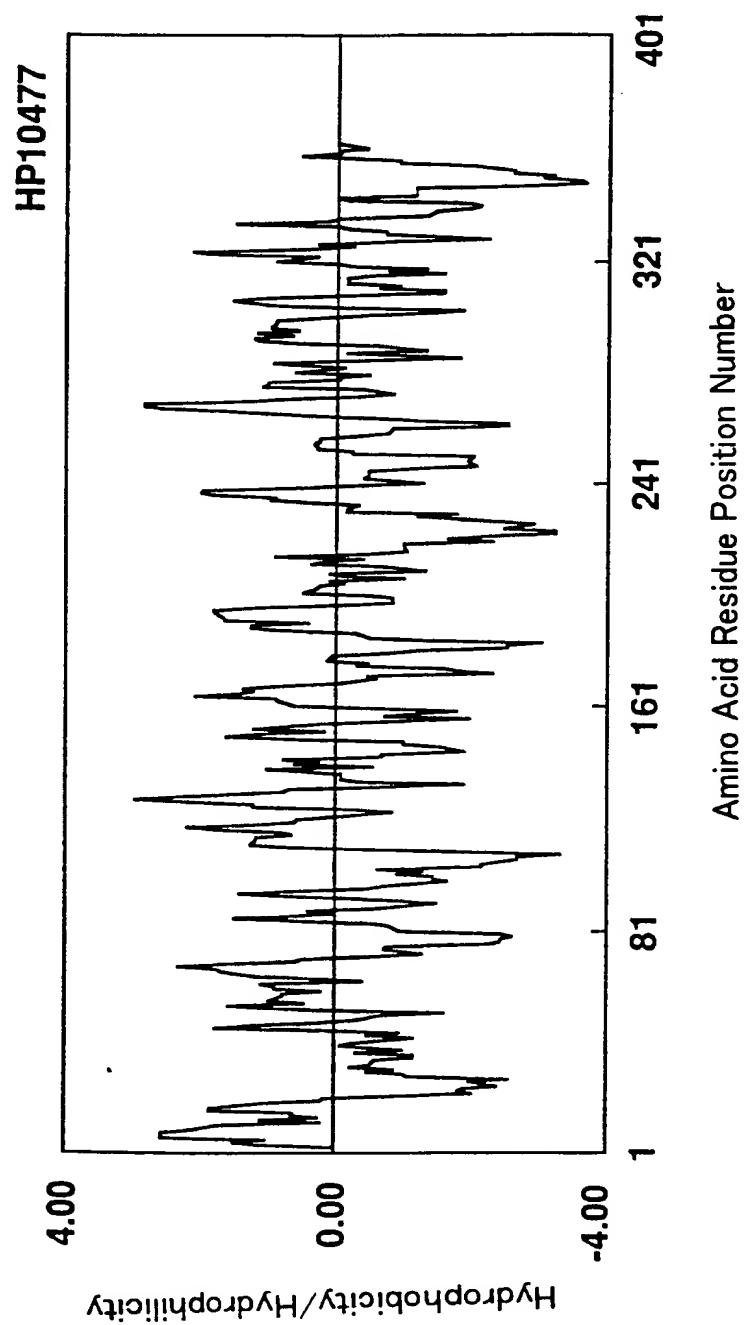


Fig. 16

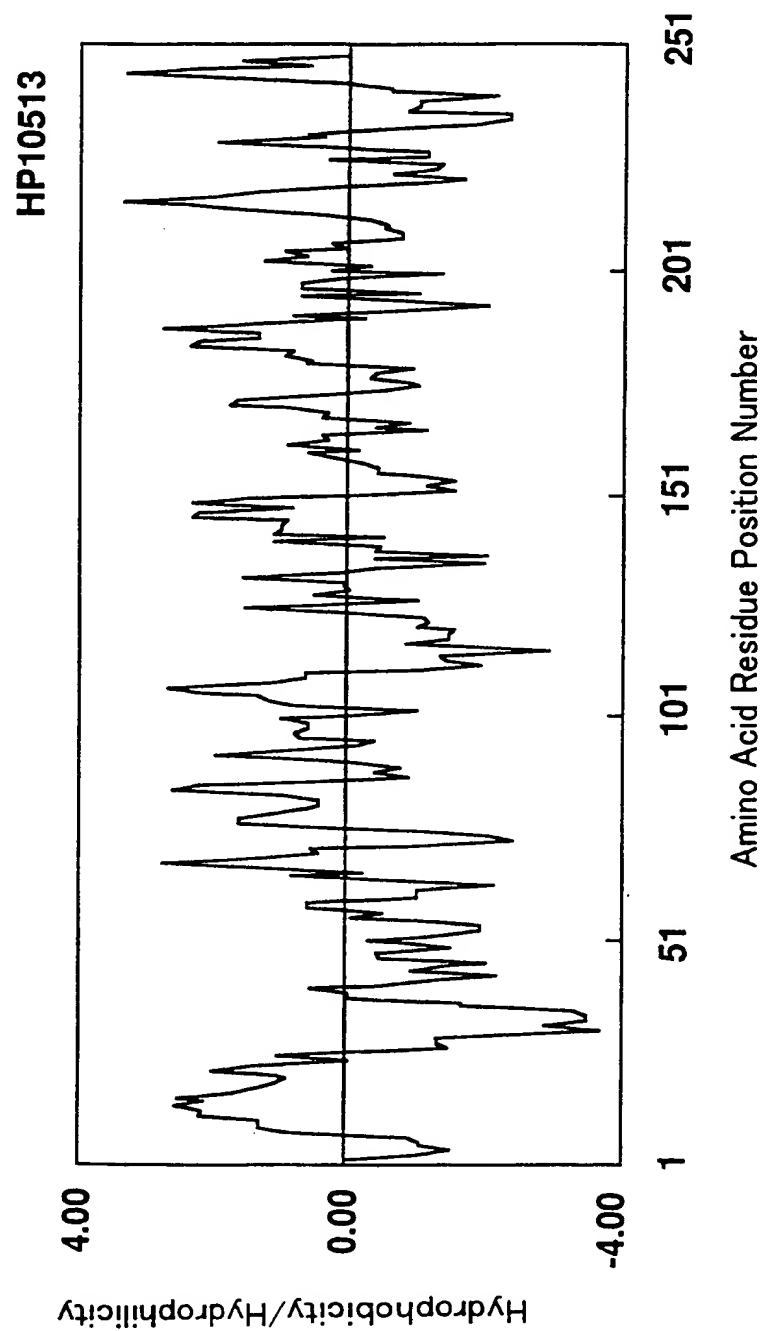


Fig.17

18/50

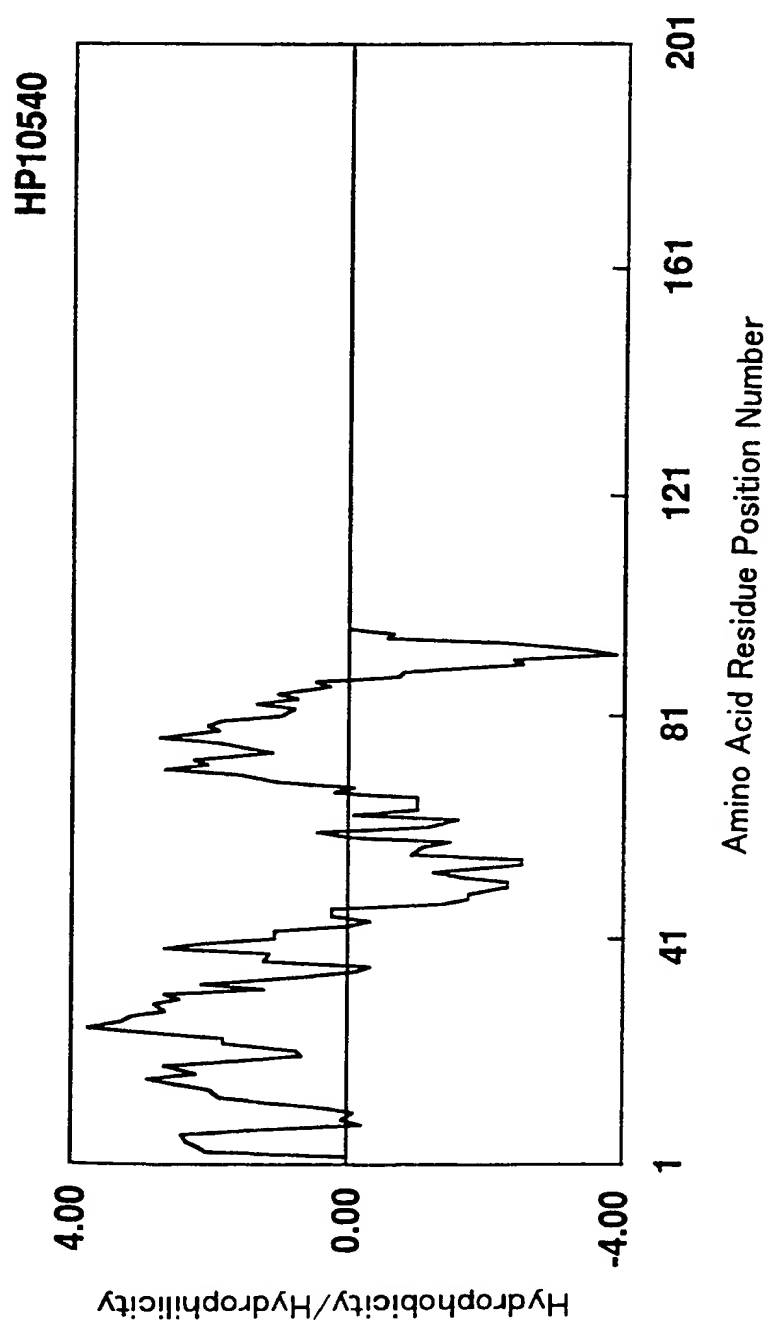


Fig. 18

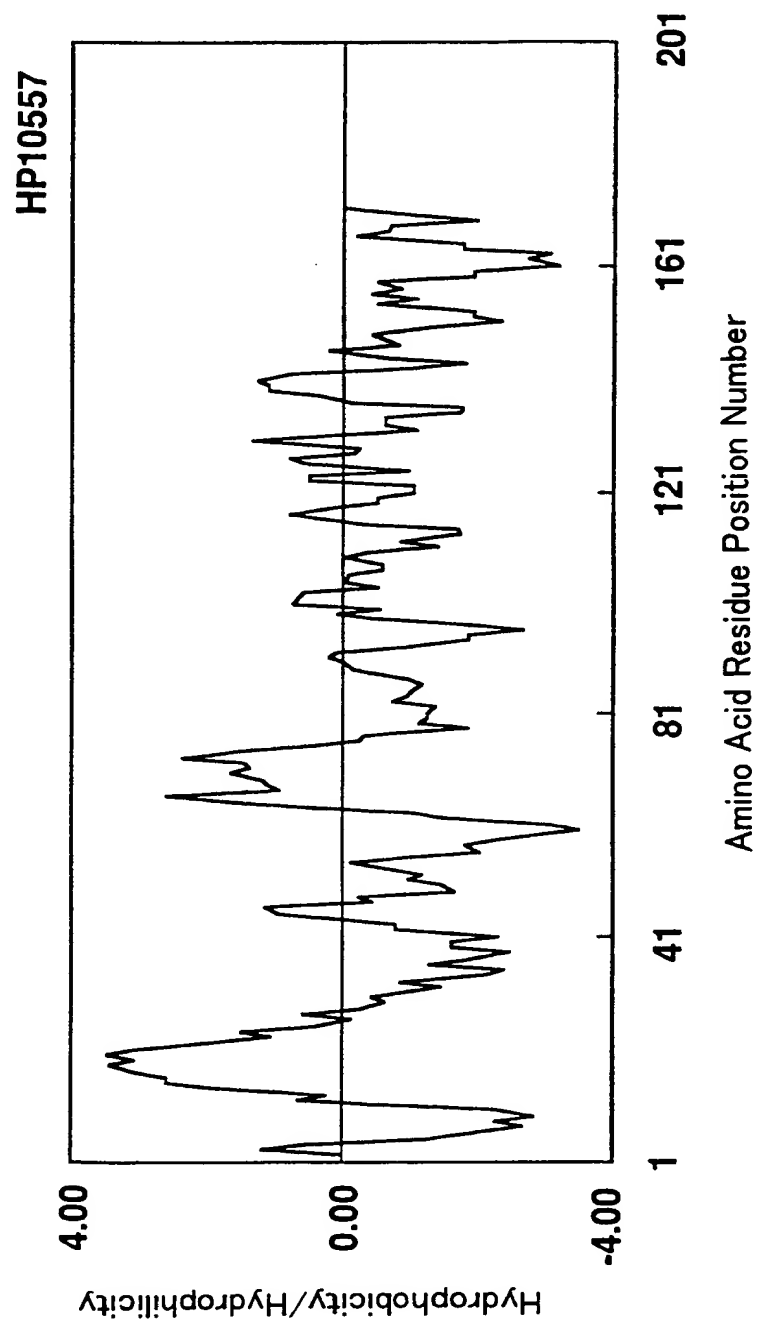


Fig. 19

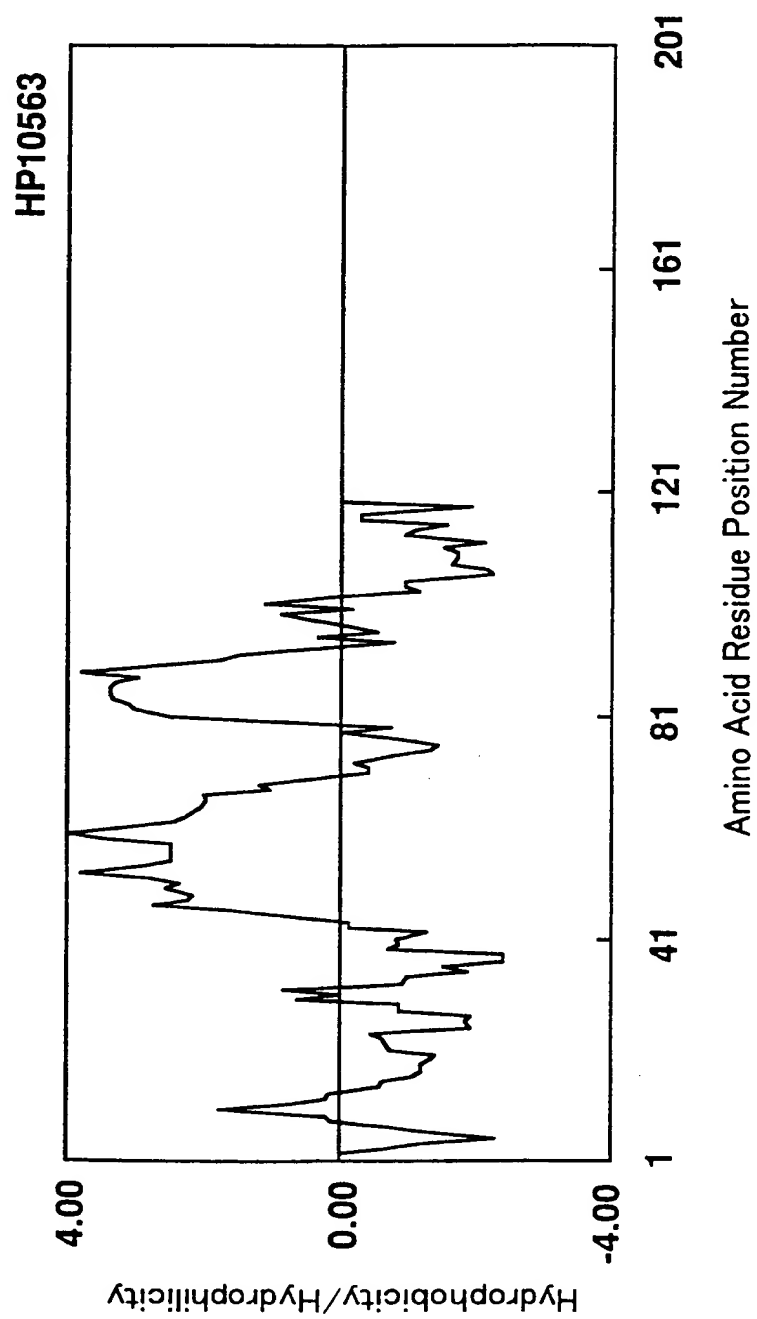


Fig. 20

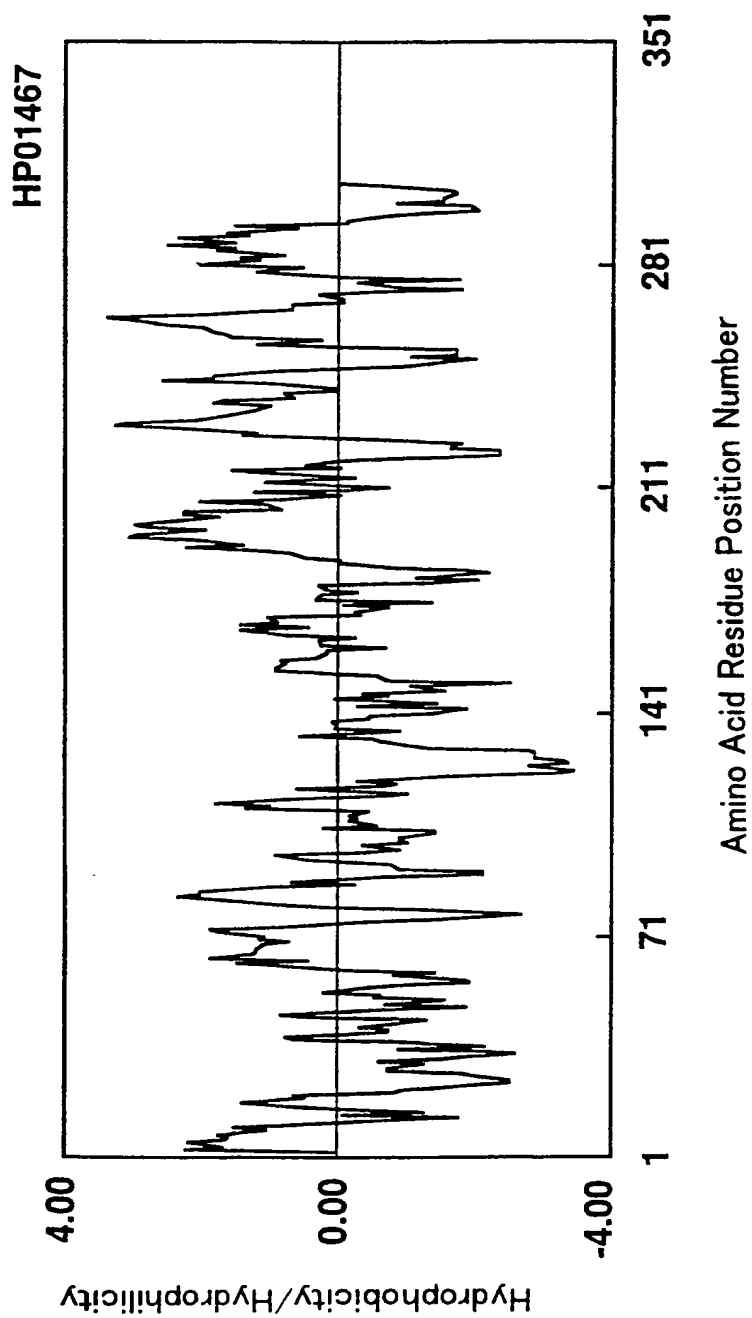


Fig. 21

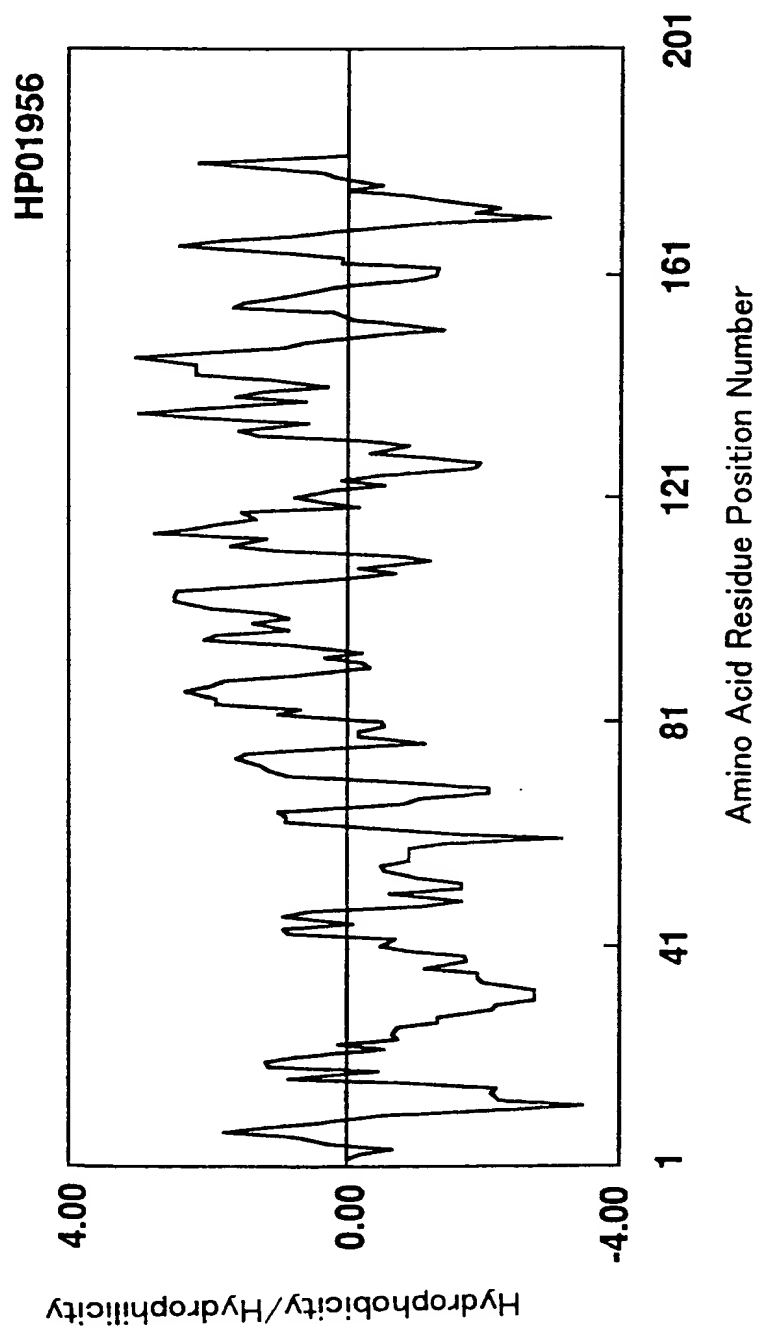


Fig.22

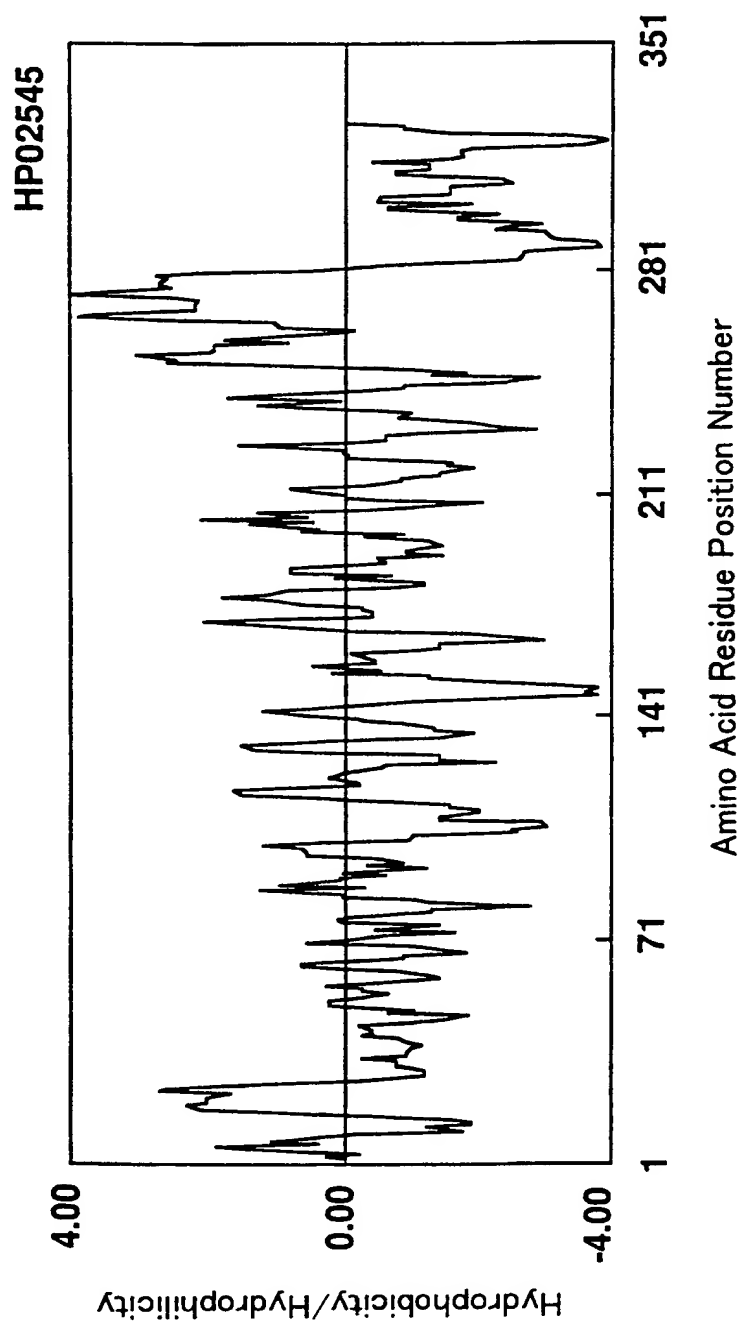


Fig. 23

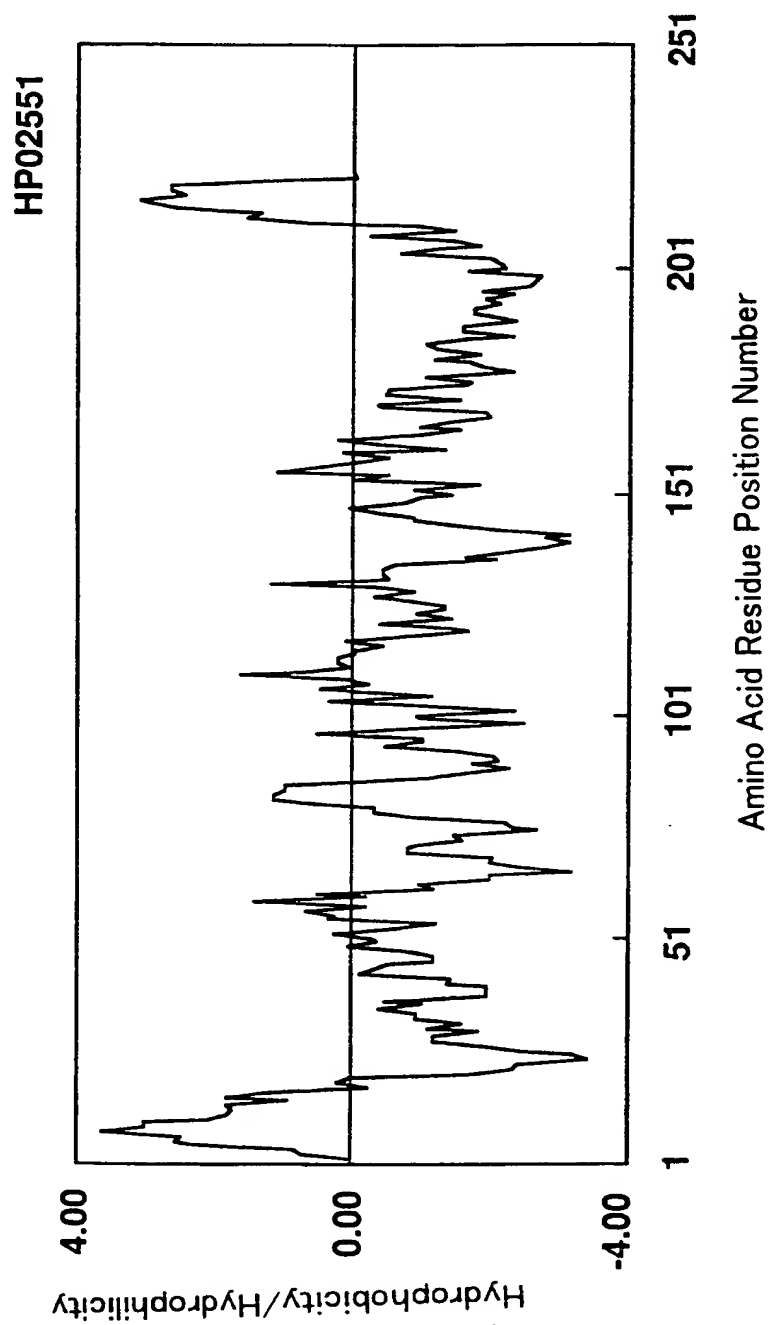


Fig. 24

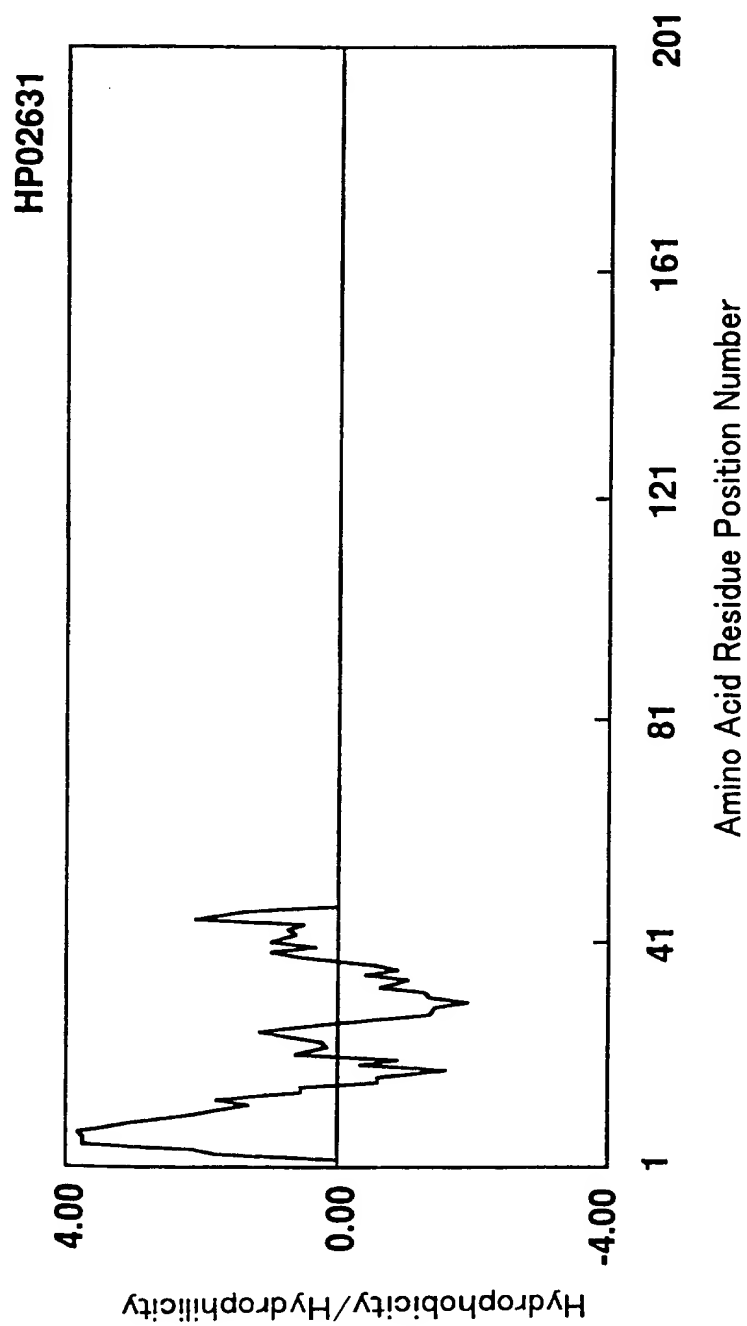


Fig. 25

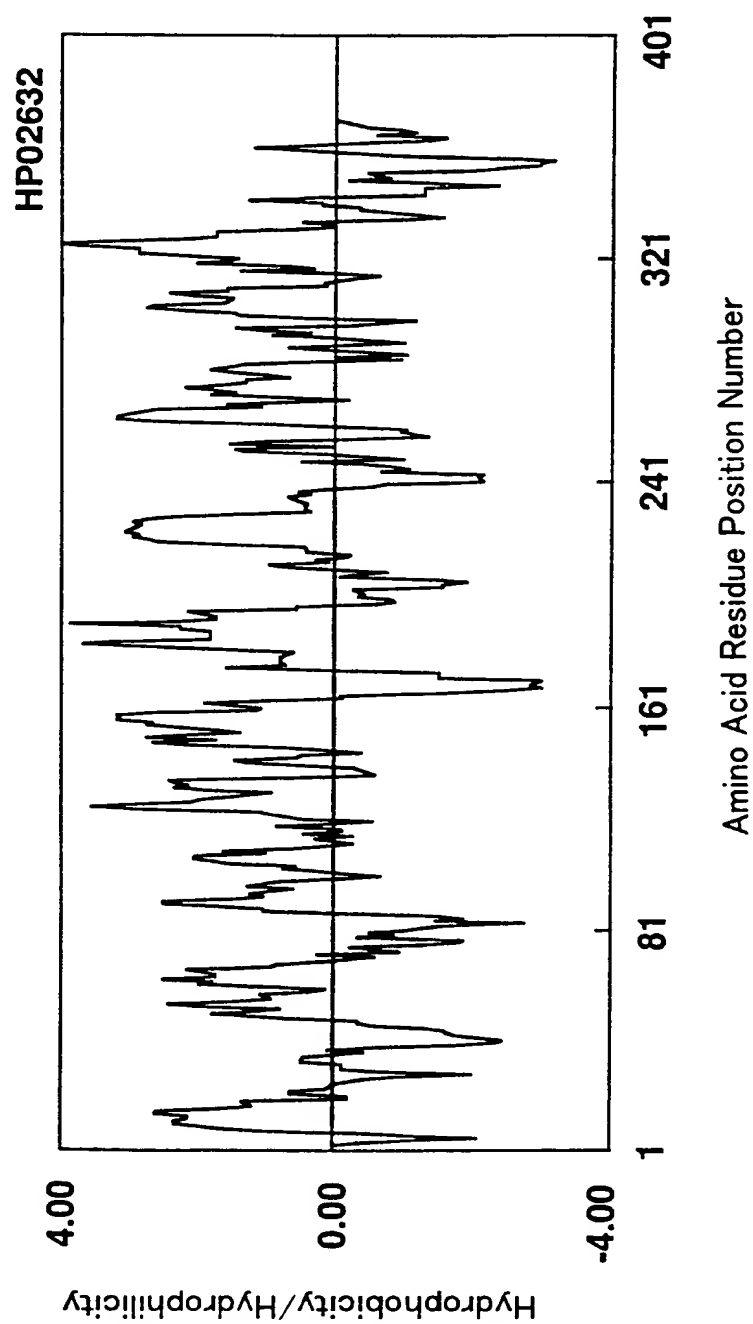


Fig. 26

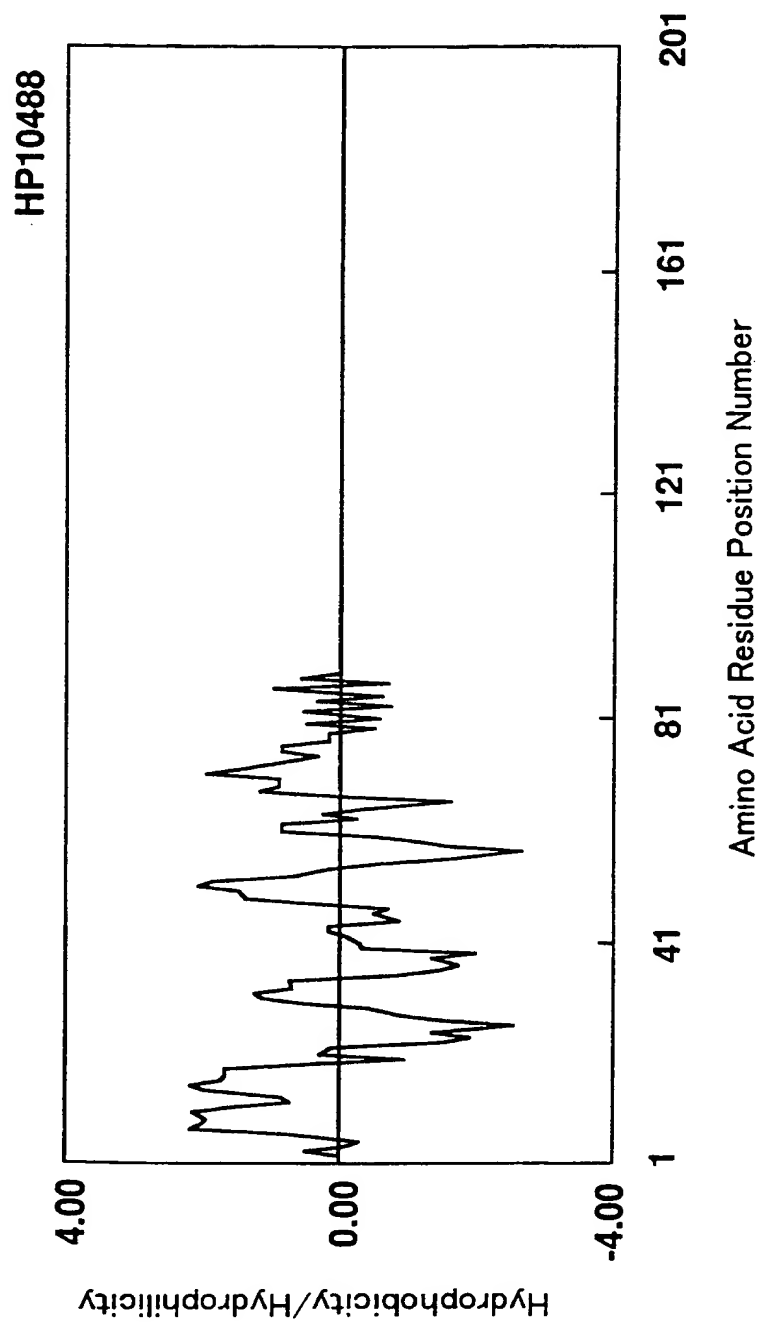


Fig.27

28/50

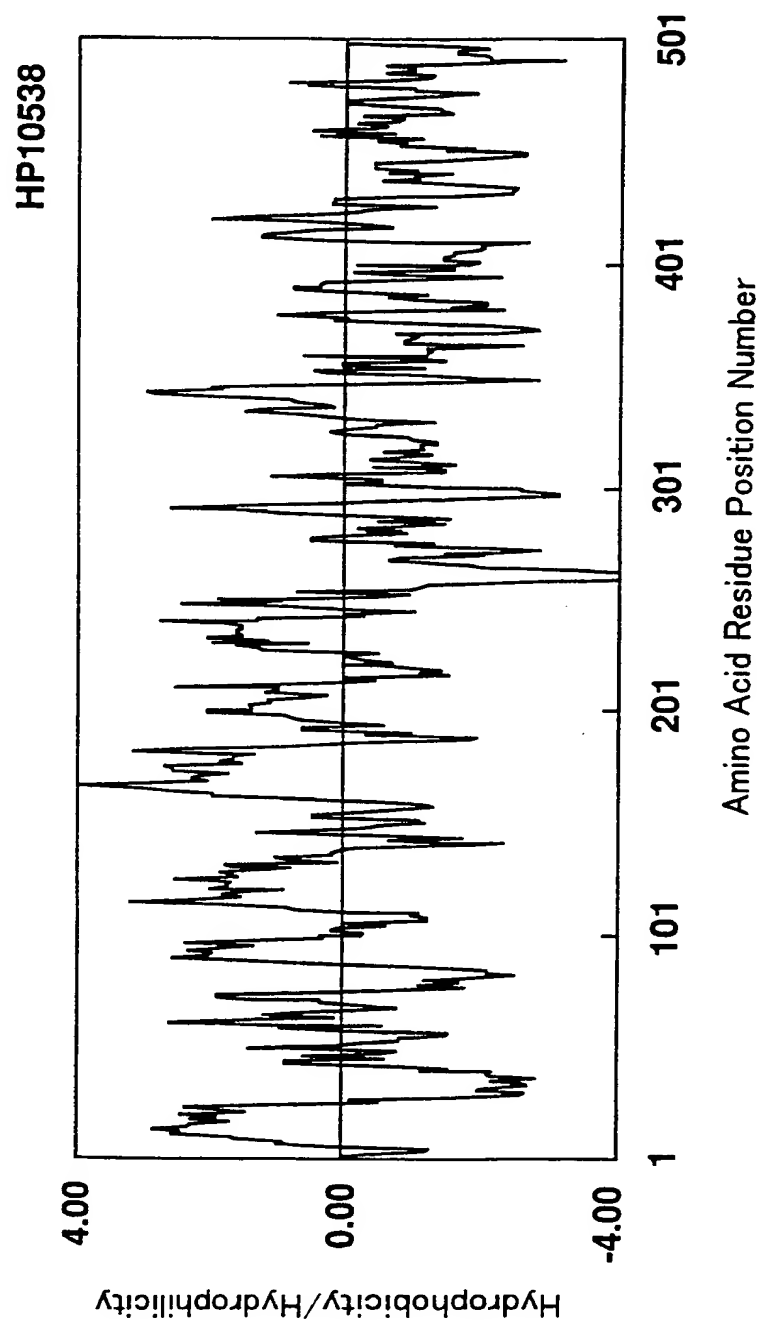


Fig. 28

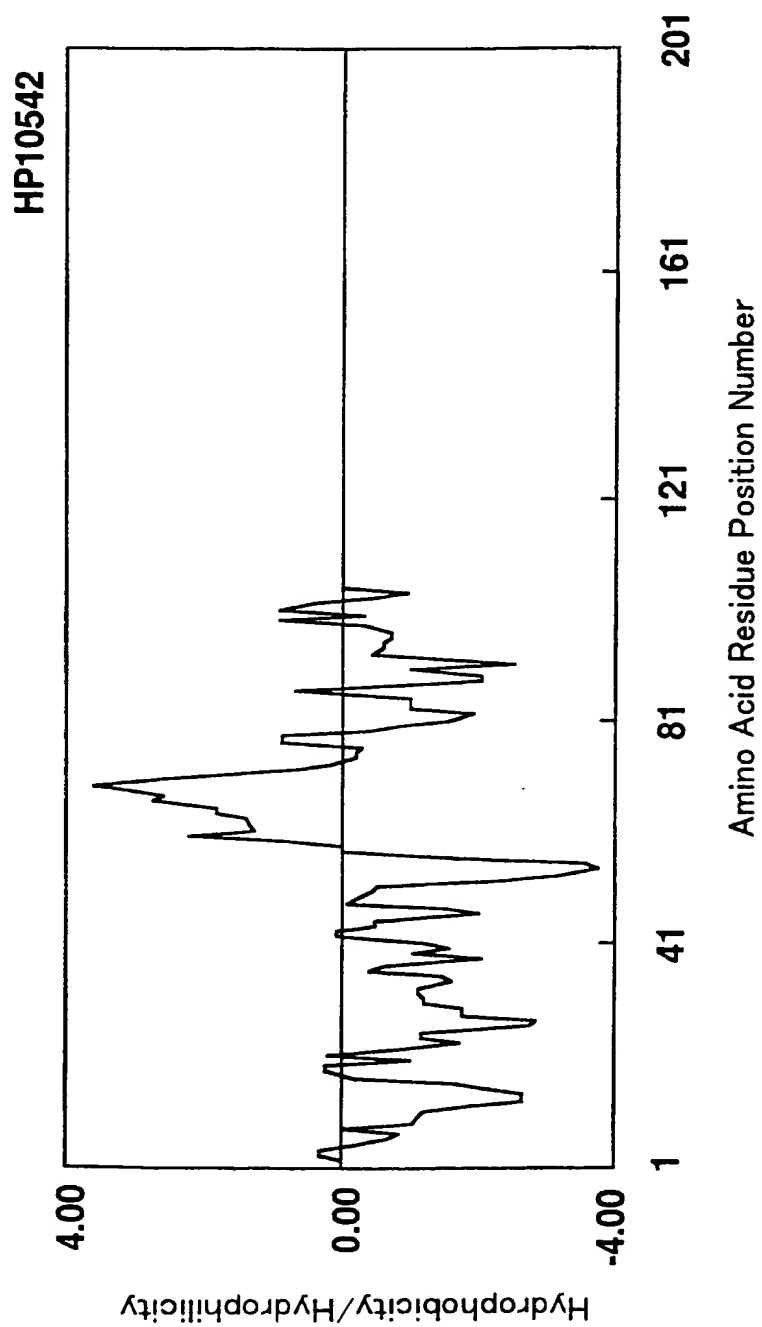


Fig. 29

30/50

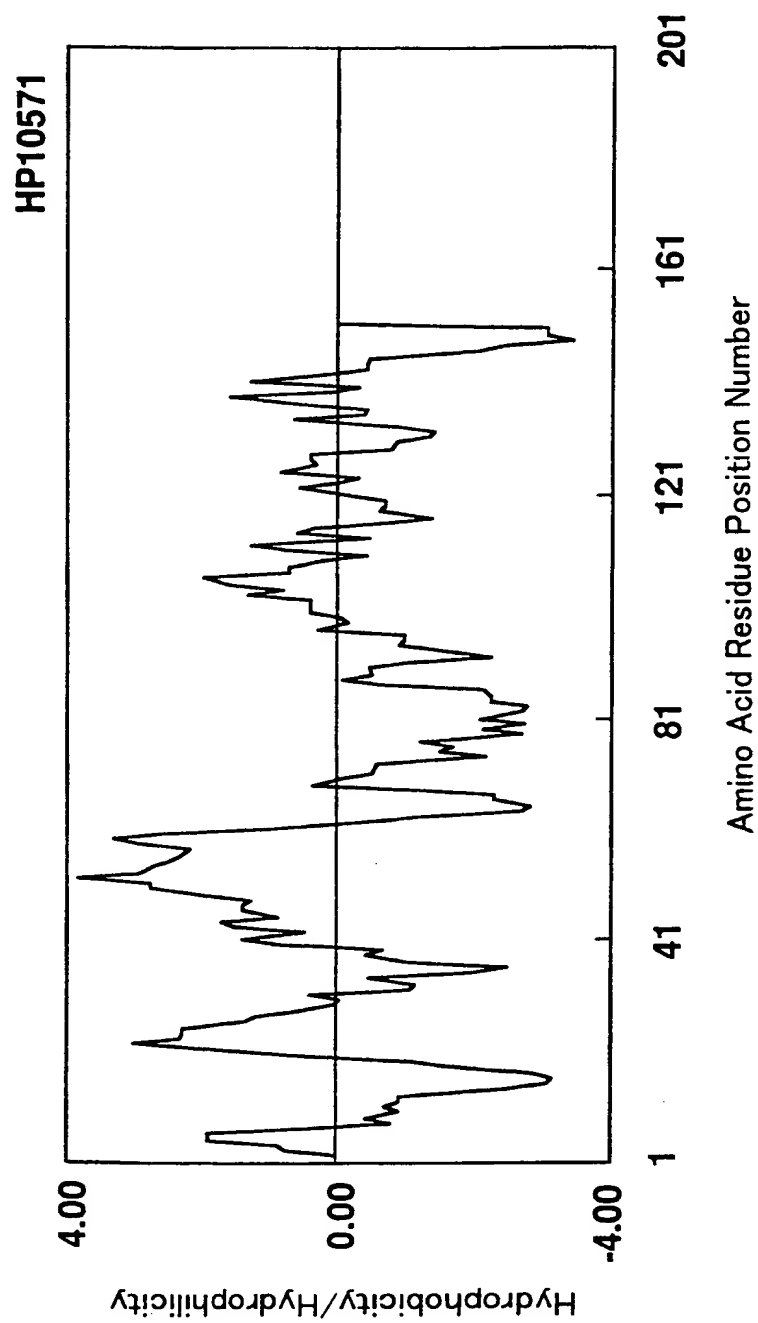


Fig. 30

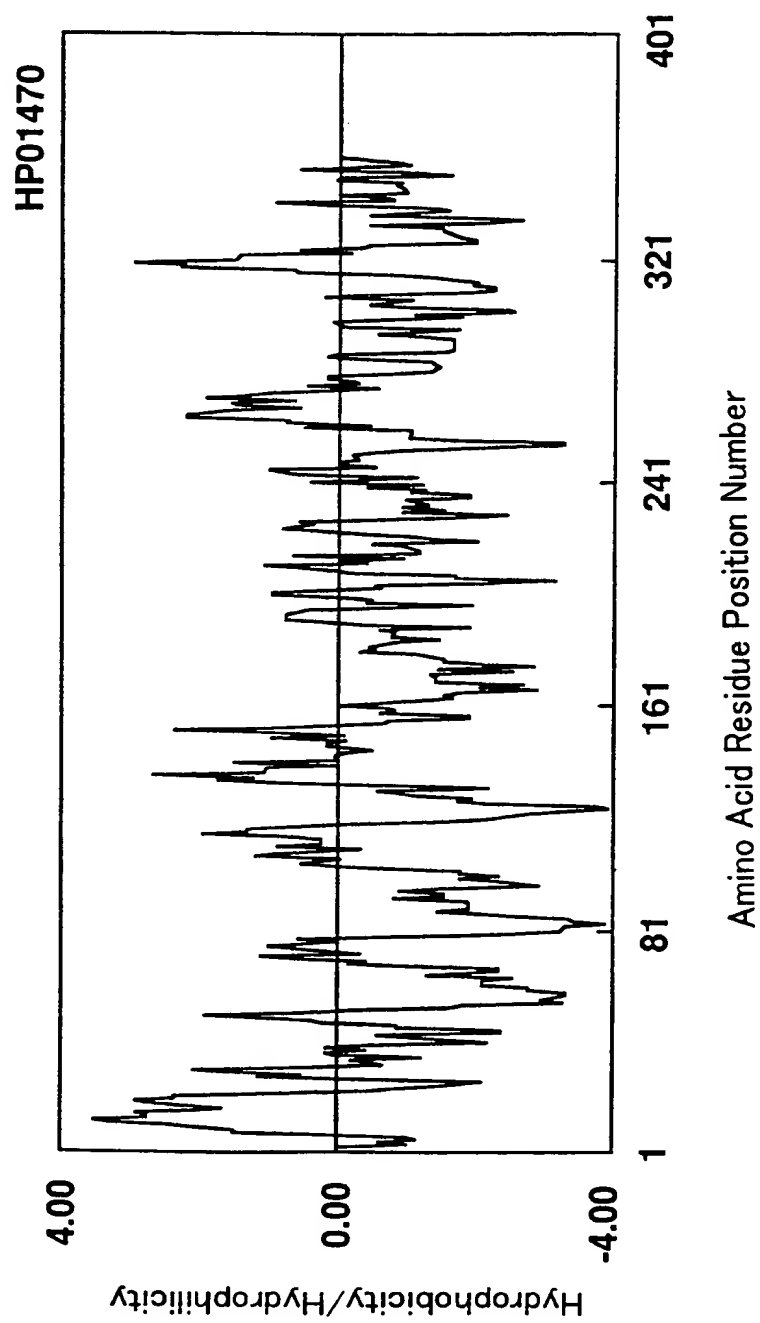


Fig. 31

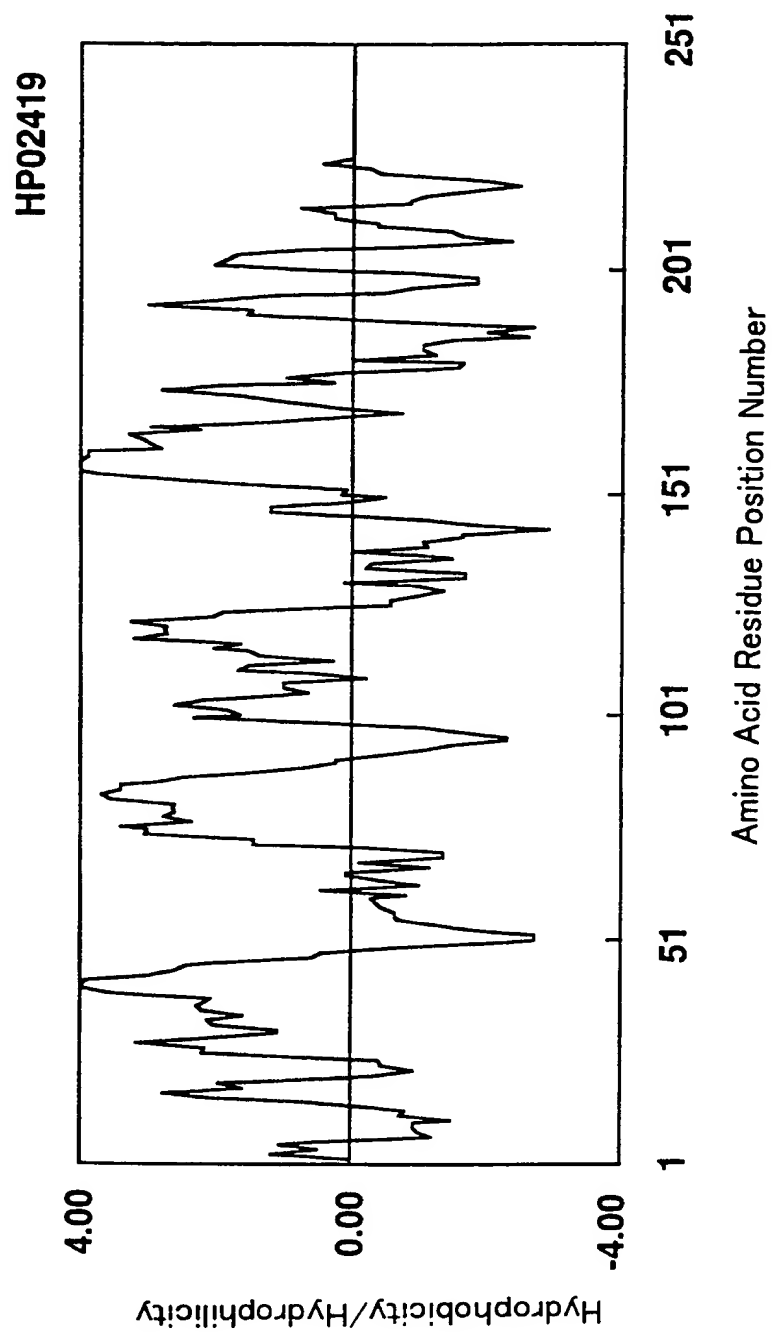


Fig.32

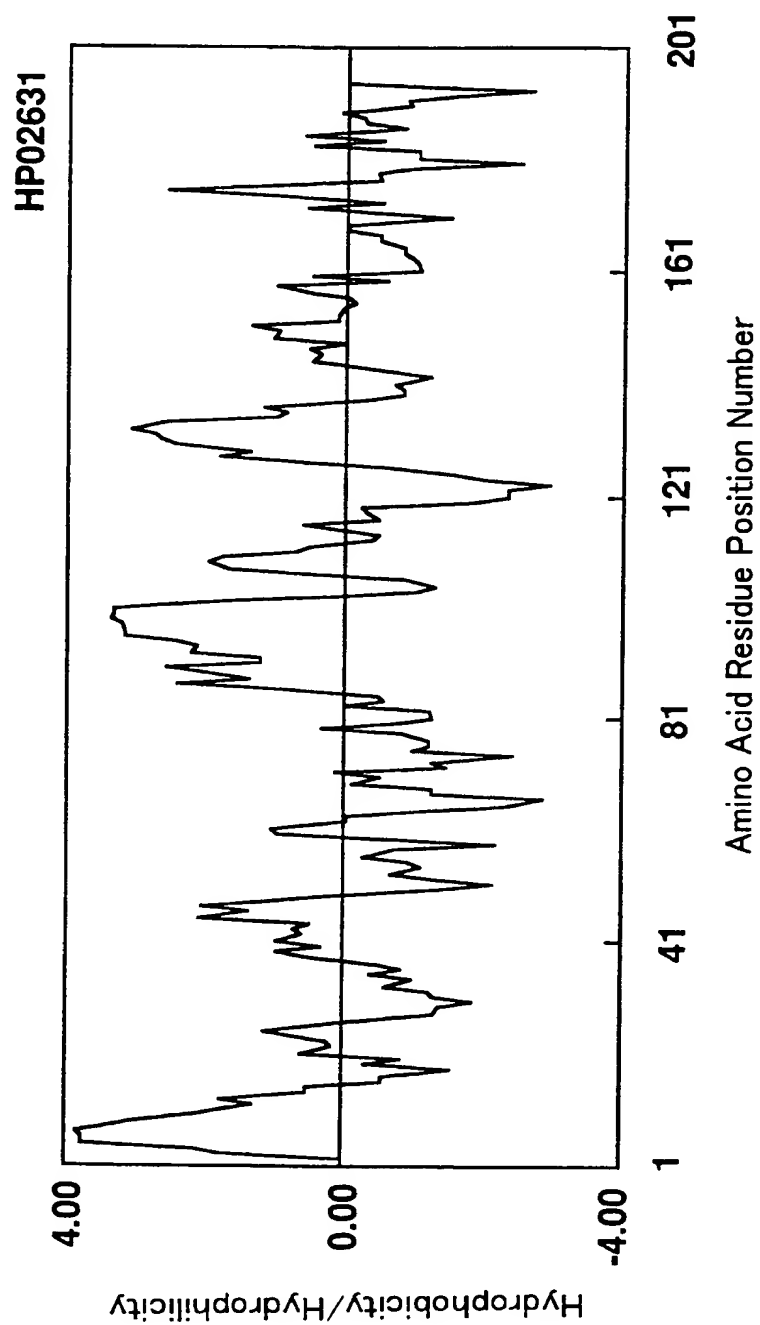


Fig. 33

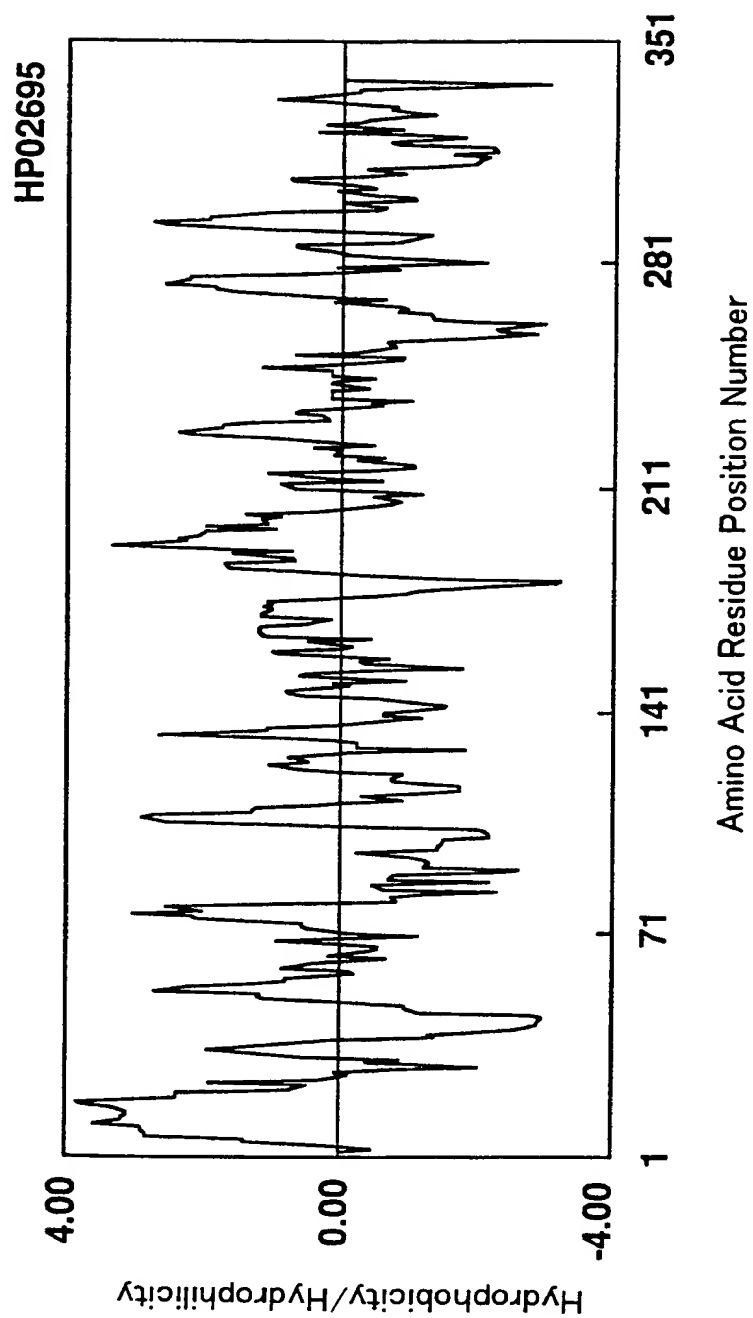


Fig. 34

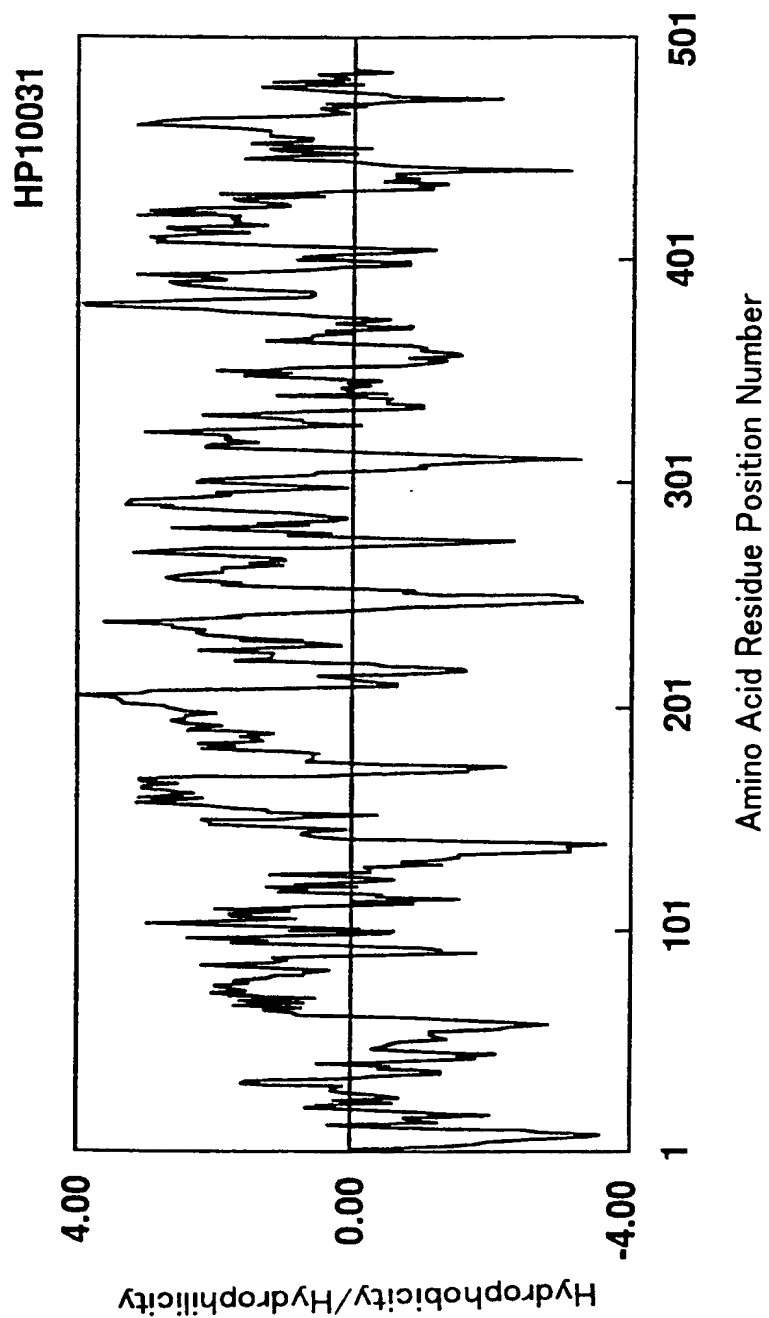


Fig. 35

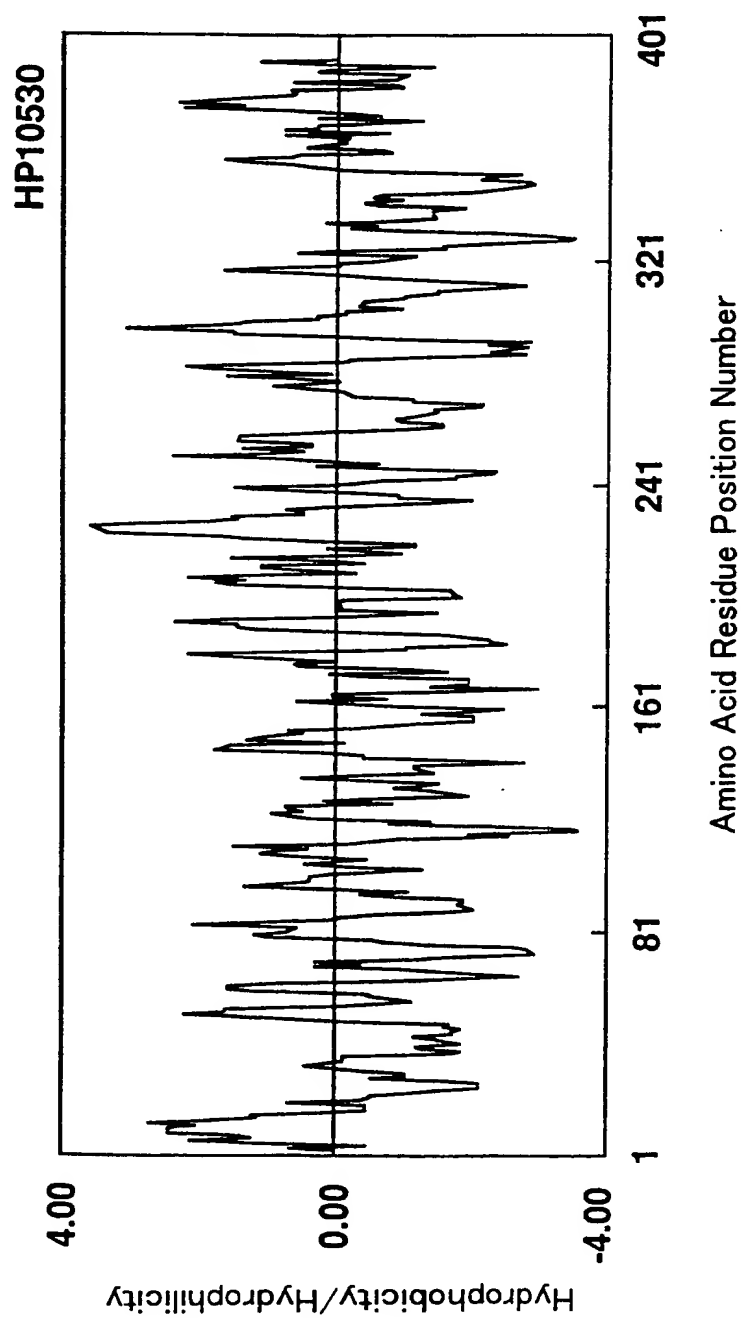


Fig. 36

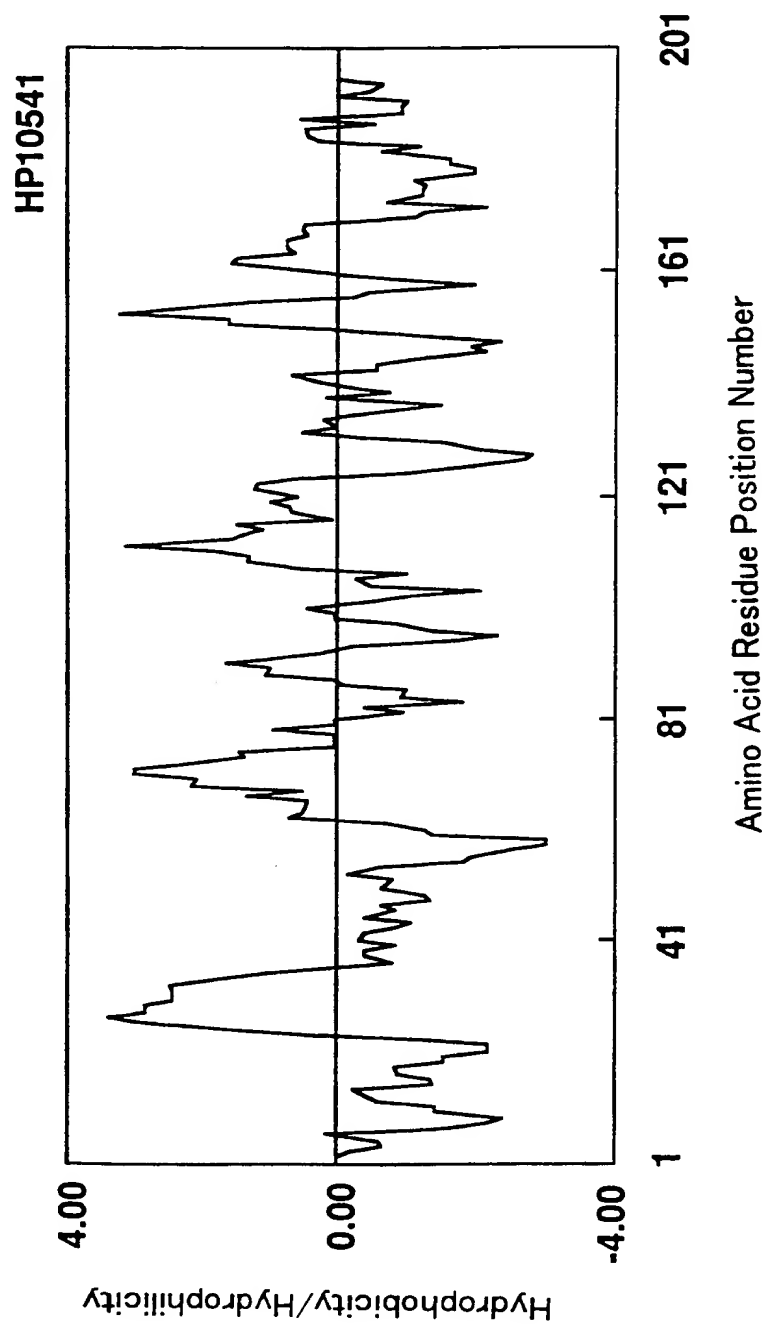


Fig.37

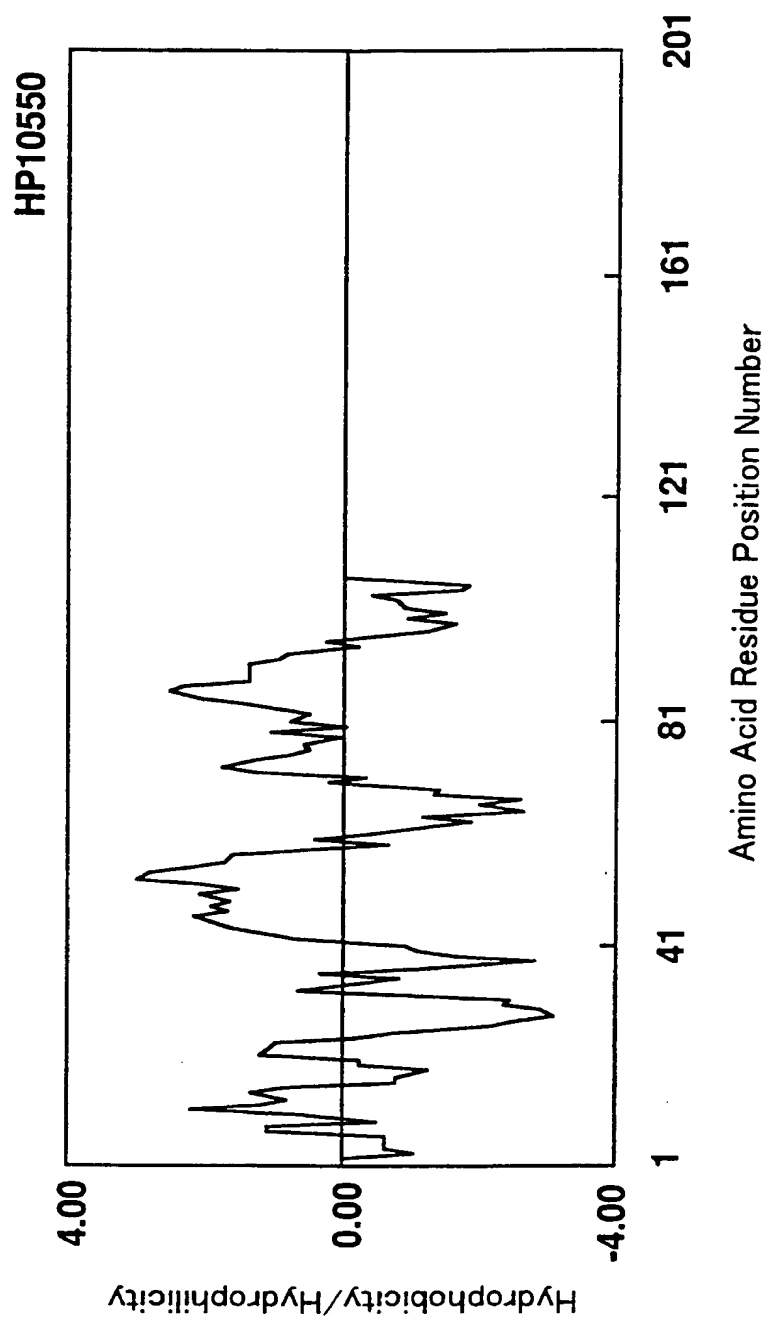


Fig. 38

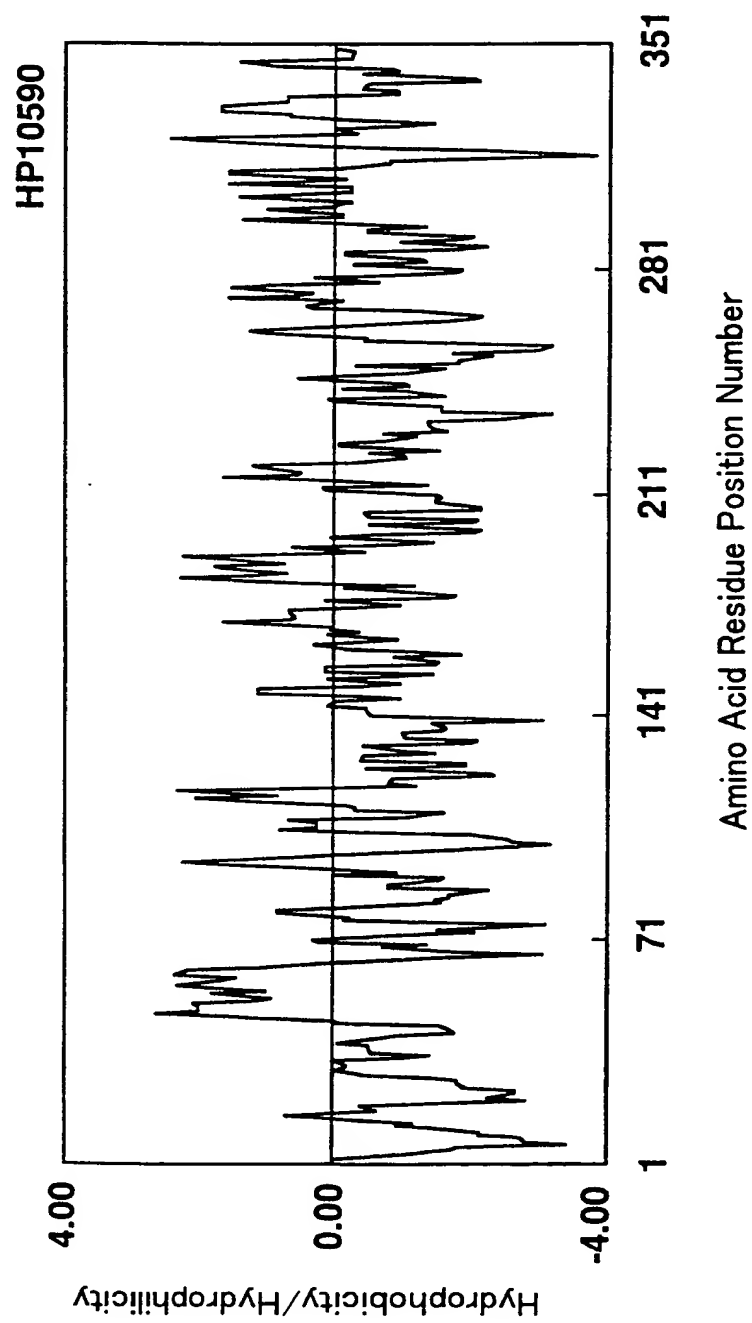


Fig. 39

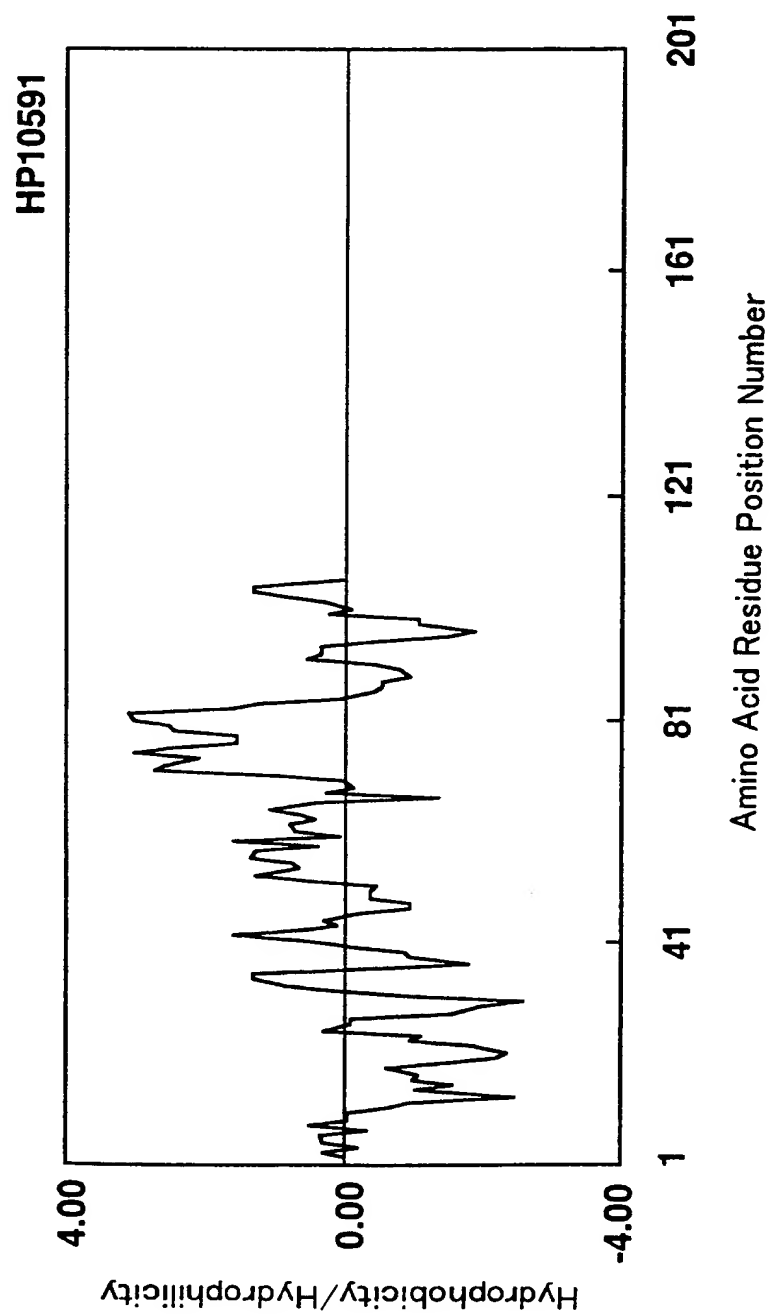


Fig. 40

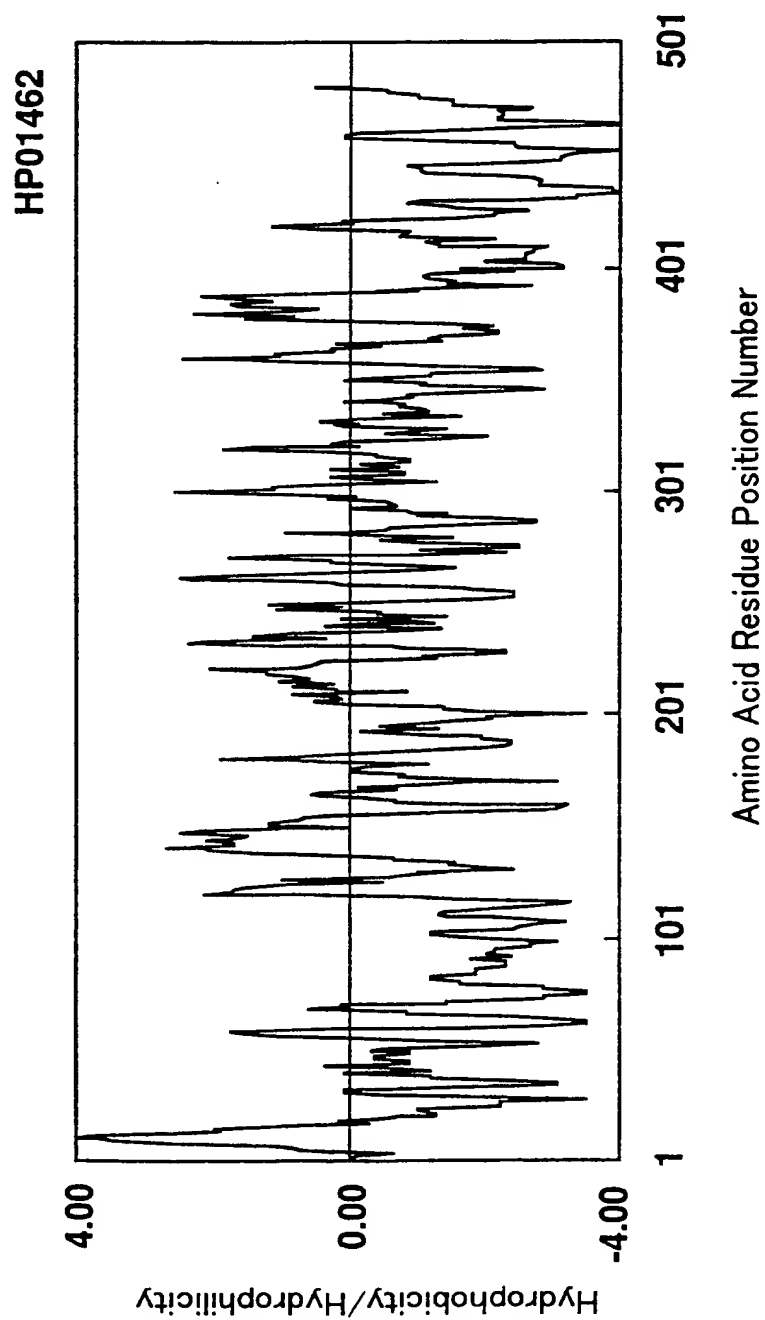


Fig. 41

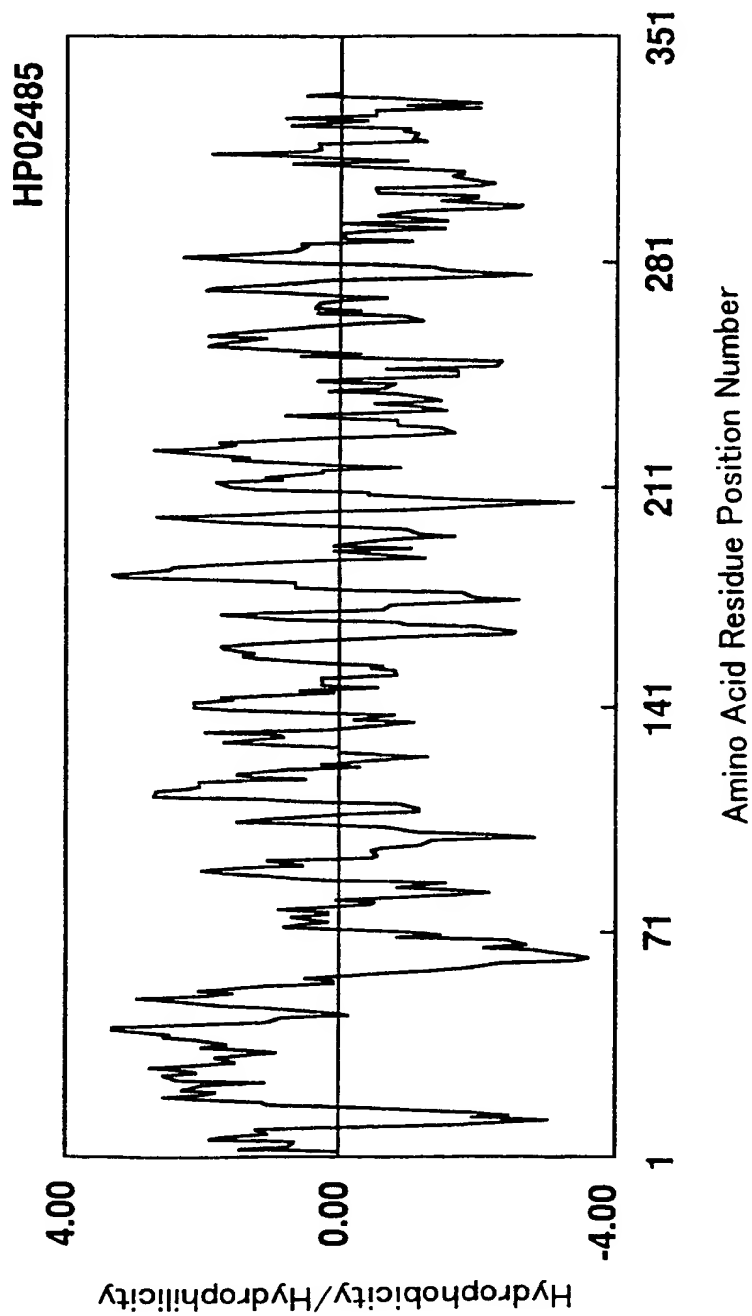


Fig.42

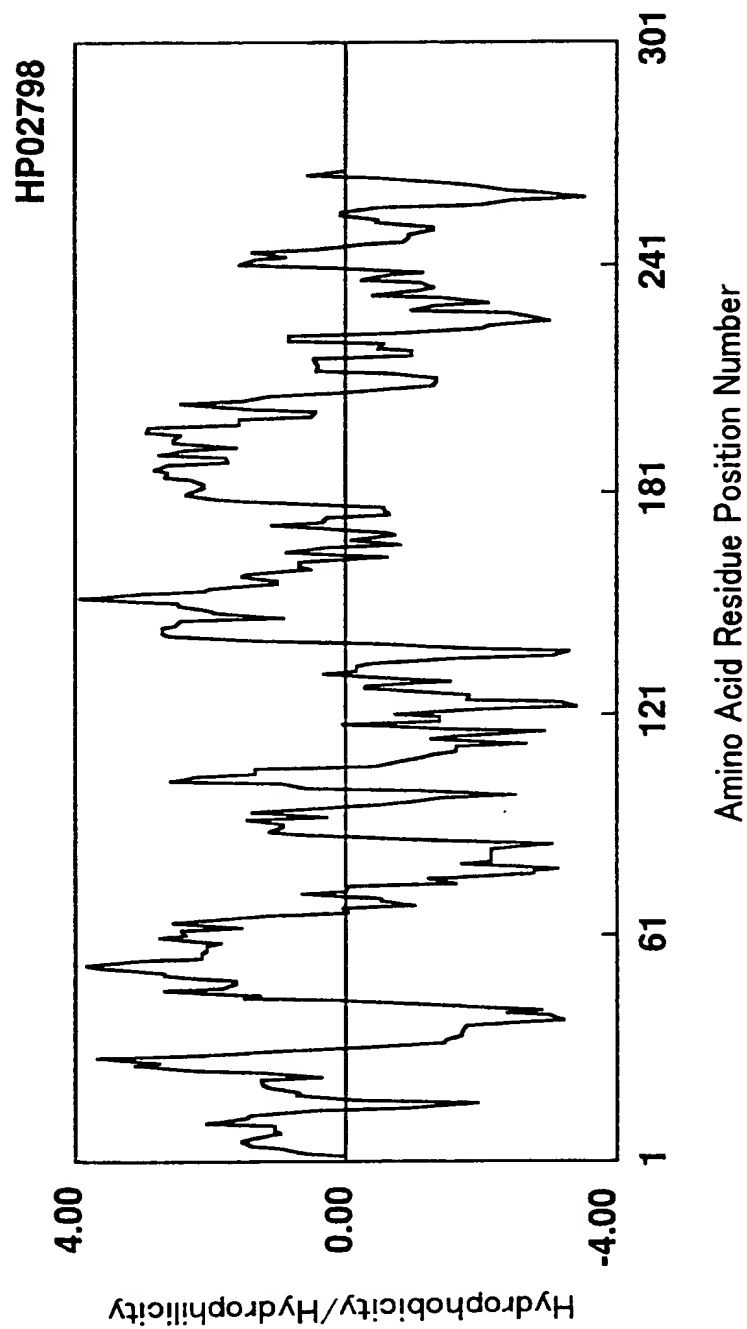


Fig. 43

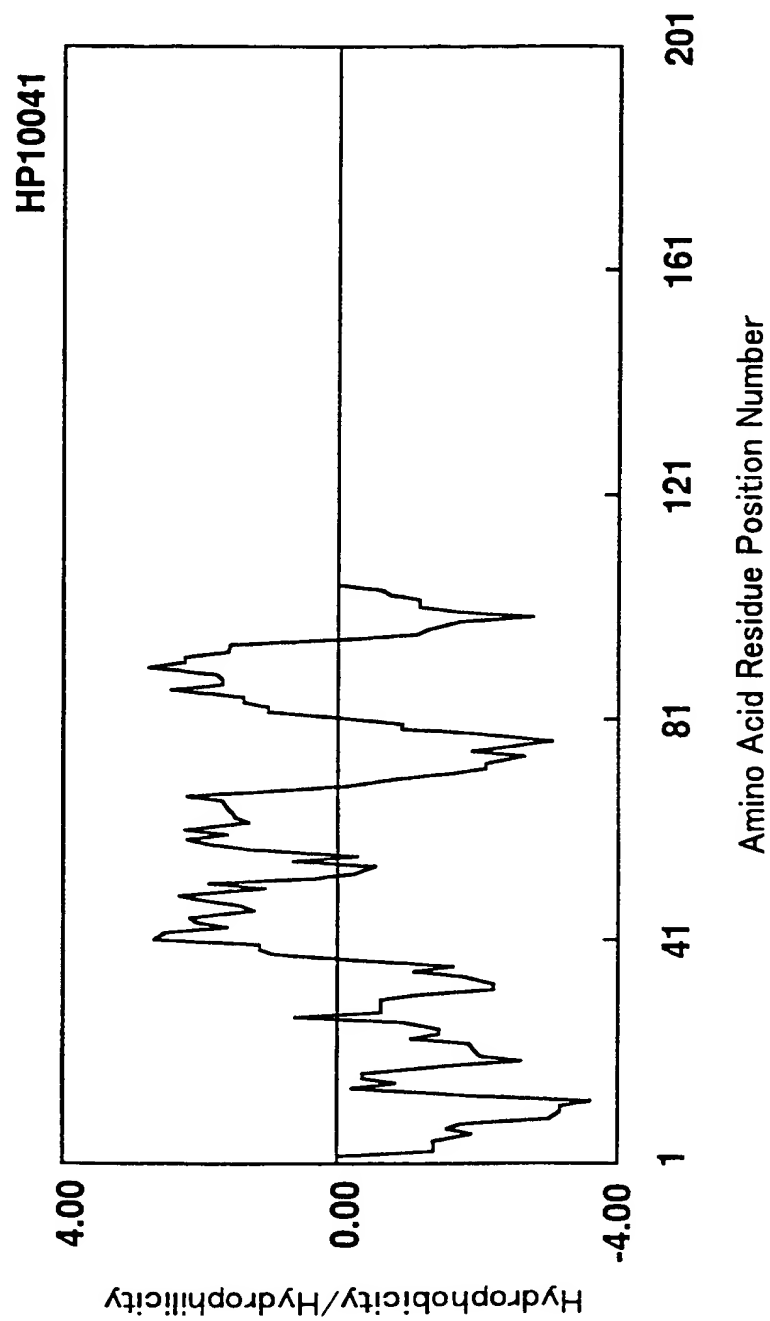


Fig. 44

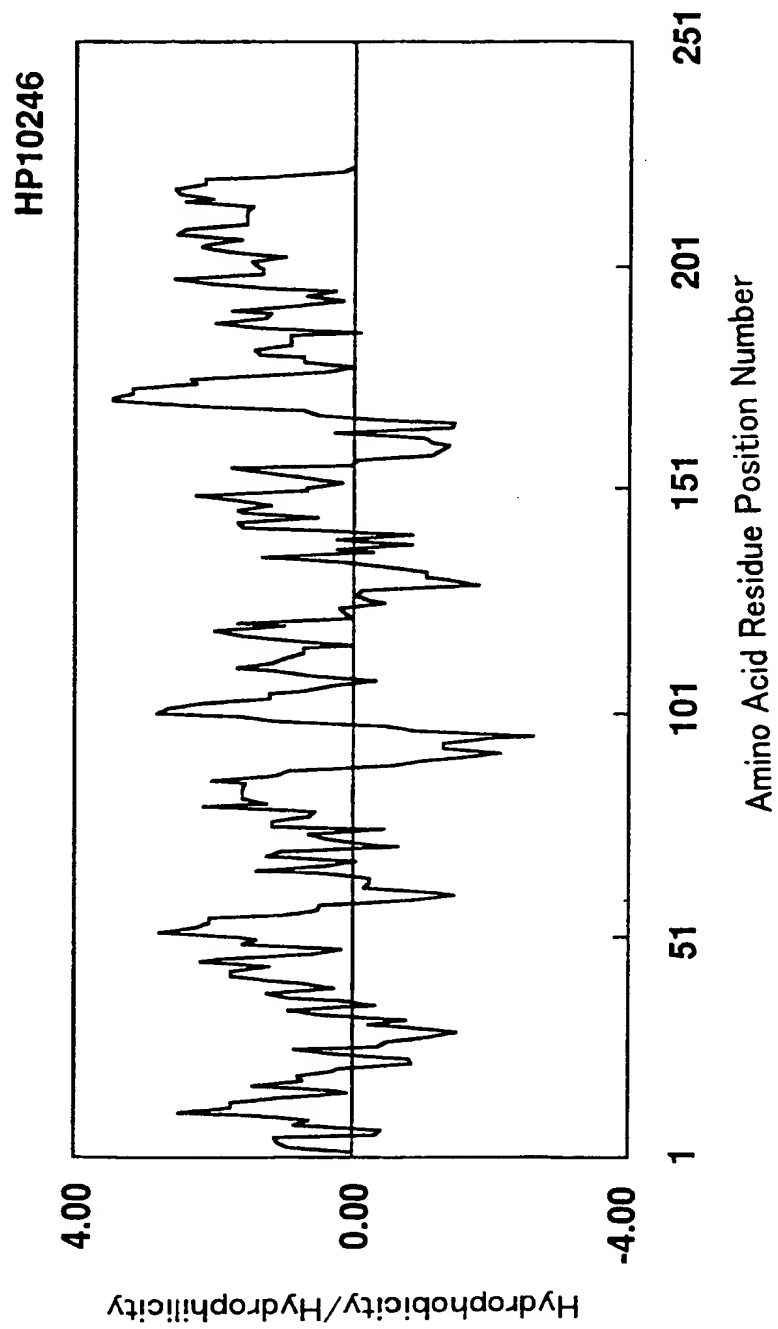


Fig. 45

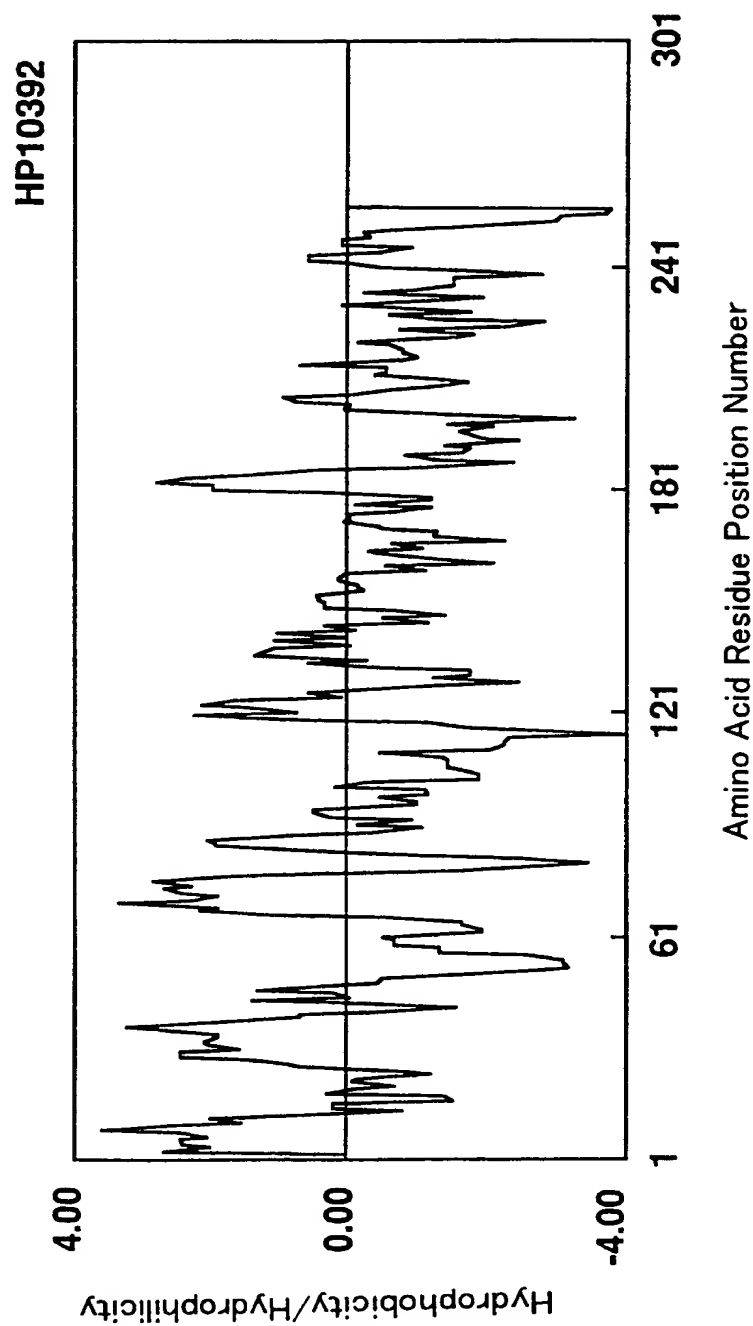


Fig. 46

47/50

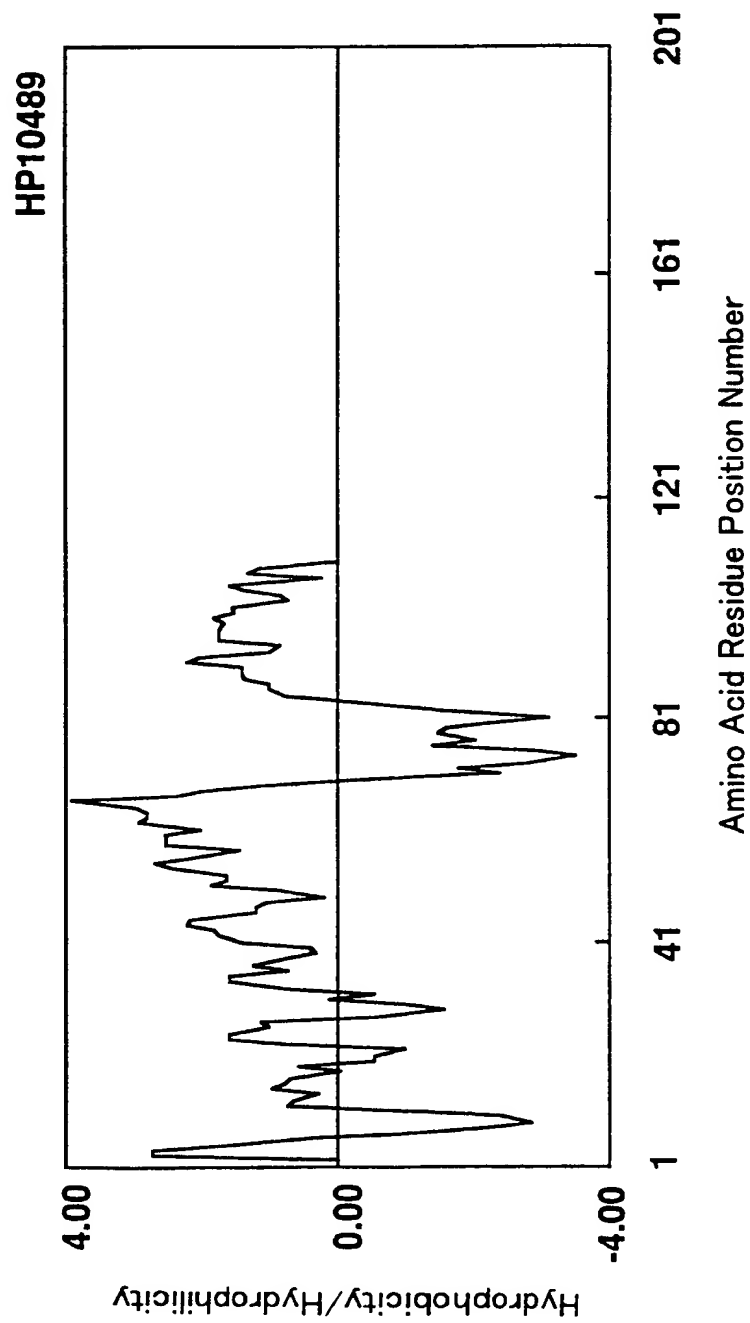


Fig.47

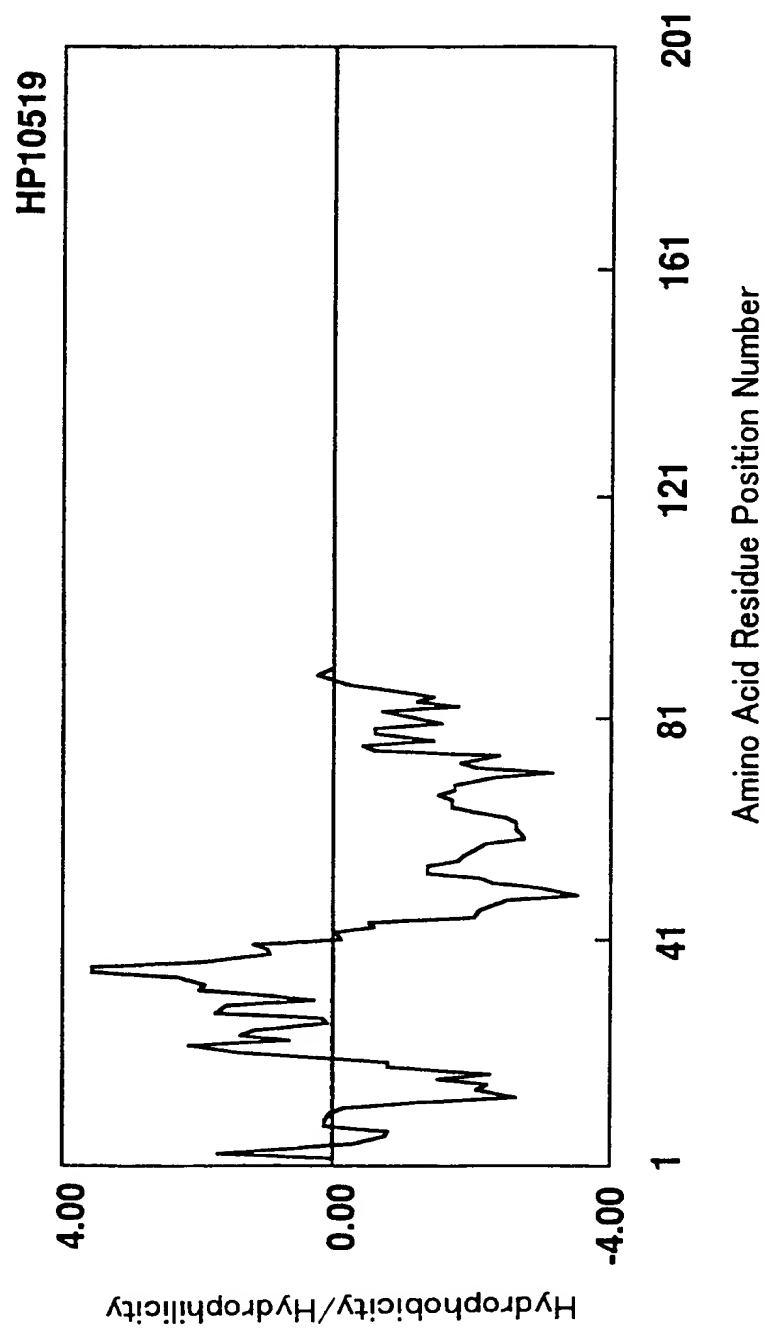


Fig. 48

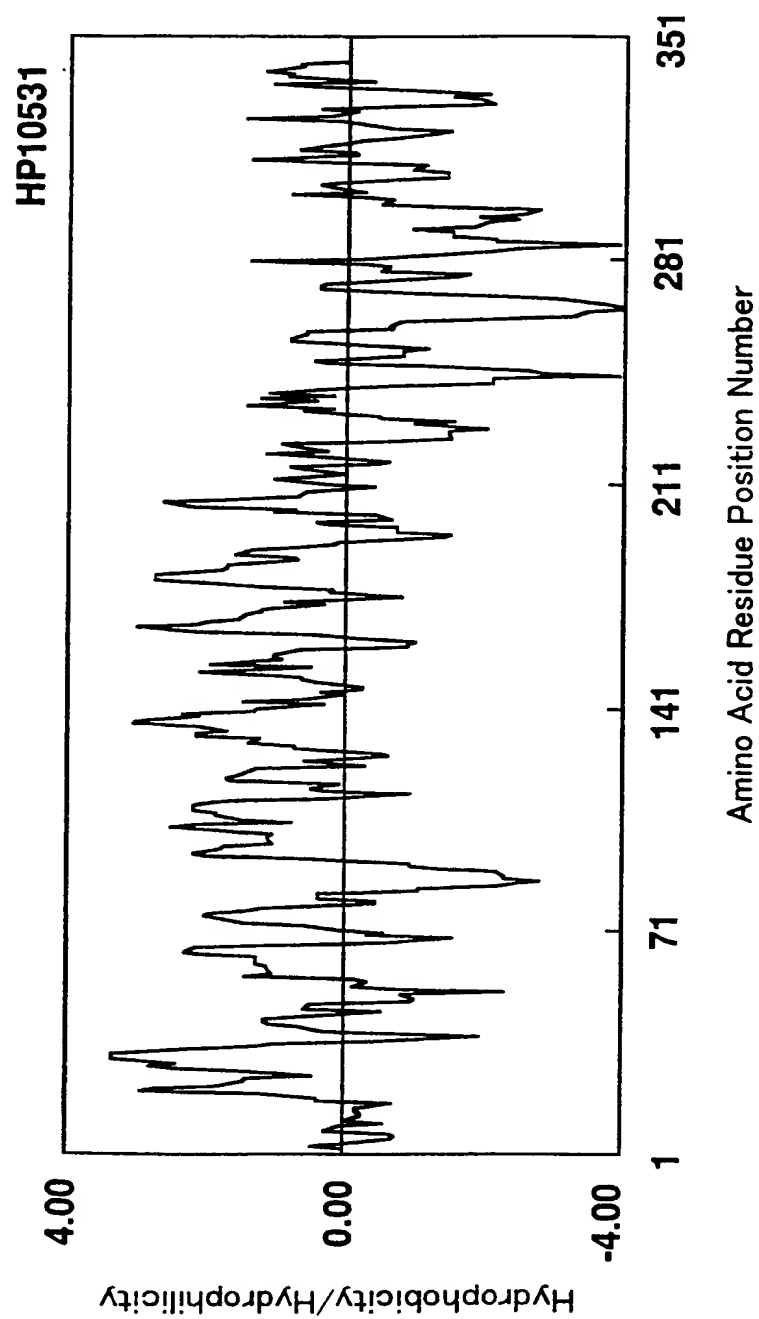


Fig. 49

50/50

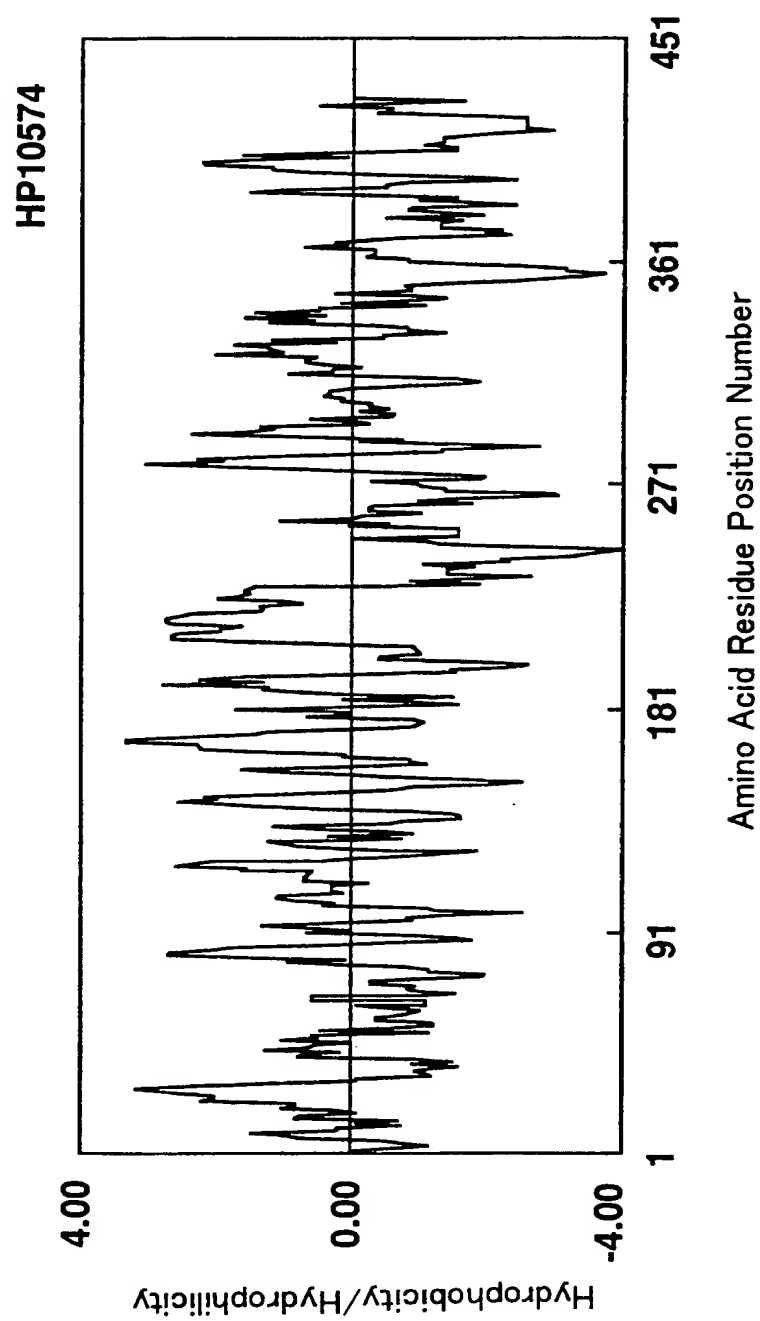


Fig. 50

1/177

Sequence listing

<110> Sagami Chemical Research Center; Protegene Inc.

5 <120> Human Proteins Having Hydrophobic Domains And DNAs Encoding These
 Proteins

 <130> 661102

10 <150> JP 10-208820
 <151> 1998-07-24

 <150> JP 10-224105
 <151> 1998-08-07

15 <150> JP 10-238116
 <151> 1998-08-25

20 <150> JP 10-254736
 <151> 1998-09-09

 <150> JP 10-275505
 <151> 1998-09-29

25 <160> 150

 <170> Windows 95 (Word 98)

 <210> 1

30 <211> 125

 <212> PRT

 <213> Homo sapiens

 <400> 1

35 Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met Gly Val Gln Val Val

	1		5		10		15									
	Gly	Arg	Ala	Phe	Ala	Arg	Ala	Leu	Arg	Gln	Glu	Phe	Ala	Ala	Ser	Arg
			20				25						30			
	Ala	Ala	Ala	Asp	Ala	Arg	Gly	Arg	Ala	Gly	His	Arg	Ser	Ala	Ala	Ala
5			35				40						45			
	Ser	Asn	Leu	Ser	Gly	Leu	Ser	Leu	Gln	Glu	Ala	Gln	Gln	Ile	Leu	Asn
			50				55						60			
	Val	Ser	Lys	Leu	Ser	Pro	Glu	Glu	Val	Gln	Lys	Asn	Tyr	Glu	His	Leu
			65				70					75				80
10	Phe	Lys	Val	Asn	Asp	Lys	Ser	Val	Gly	Gly	Ser	Phe	Tyr	Leu	Gln	Ser
					85					90					95	
	Lys	Val	Val	Arg	Ala	Lys	Glu	Arg	Leu	Asp	Glu	Glu	Leu	Lys	Ile	Gln
					100					105					110	
	Ala	Gln	Glu	Asp	Arg	Glu	Lys	Gly	Gln	Met	Pro	His	Thr			
15					115					120					125	

<211> 131

<212> PRT

20 <213> Homo sapiens

<400> 2

	Met	Ala	Gly	Ile	Lys	Ala	Leu	Ile	Ser	Leu	Ser	Phe	Gly	Gly	Ala	Ile
	1				5					10					15	
25	Gly	Leu	Met	Phe	Leu	Met	Leu	Gly	Cys	Ala	Leu	Pro	Ile	Tyr	Asn	Lys
				20					25					30		
	Tyr	Trp	Pro	Leu	Phe	Val	Leu	Phe	Phe	Tyr	Ile	Leu	Ser	Pro	Ile	Pro
			35					40					45			
	Tyr	Cys	Ile	Ala	Arg	Arg	Leu	Val	Asp	Asp	Thr	Asp	Ala	Met	Ser	Asn
30		50					55					60				
	Ala	Cys	Lys	Glu	Leu	Ala	Ile	Phe	Leu	Thr	Thr	Gly	Ile	Val	Val	Ser
	65					70				75					80	
	Ala	Phe	Gly	Leu	Pro	Ile	Val	Phe	Ala	Arg	Ala	His	Leu	Ile	Glu	Trp
				85					90					95		
35	Gly	Ala	Cys	Ala	Leu	Val	Leu	Thr	Gly	Asn	Thr	Val	Ile	Phe	Ala	Thr

3/177

100 105 110
 Ile Leu Gly Phe Phe Leu Val Phe Gly Ser Asn Asp Asp Phe Ser Trp
 115 120 125
 Gln Gln Trp
 5 130

 <210> 3
 <211> 242
 <212> PRT
 10 <213> Homo sapiens

 <400> 3
 Met Ala Lys His Glu Gln Ile Leu Val Leu Asp Pro Pro Thr Asp Leu
 1 5 10 15
 15 Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu Lys Leu
 20 25 30
 Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys Val Lys Thr Thr Ala
 35 40 45
 Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile Ile Asp Pro Gly
 20 50 55 60
 Ser Thr Val Thr Val Ser Val Met Leu Gln Pro Phe Asp Tyr Asp Pro
 65 70 75 80
 Asn Glu Lys Ser Lys His Lys Phe Met Val Gln Thr Ile Phe Ala Pro
 85 90 95
 25 Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys Glu Ala Lys Pro Asp
 100 105 110
 Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe Glu Met Pro Asn Glu
 115 120 125
 Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys Ala Val Pro Leu Asn
 30 130 135 140
 Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro His Ser Val Ser Leu
 145 150 155 160
 Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu Cys Lys Arg Leu Gln
 165 170 175
 35 Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg His Leu Arg Asp Glu

4/177

	180	185	190
	Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp Lys Pro Gly Ser Thr		
	195	200	205
	Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser Pro Leu Pro Ser Leu		
5	210	215	220
	Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe Phe Leu Gly Lys Phe		
	225	230	235
	Ile Leu		240
10	<210> 4		
	<211> 264		
	<212> PRT		
	<213> Homo sapiens		
15	<400> 4		
	Met Phe Val Pro Cys Gly Glu Ser Ala Pro Asp Leu Ala Gly Phe Thr		
	1	5	10
	Leu Leu Met Pro Ala Val Ser Val Gly Asn Val Gly Gln Leu Ala Met		15
	20	25	30
20	Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys Ile Gly Tyr Phe Tyr		
	35	40	45
	Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn Pro Tyr Ala Thr Thr		
	50	55	60
	Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala Glu Val Tyr Ser Leu		
25	65	70	75
	Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg Ser Ile Phe Ile Lys		80
	85	90	95
	Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu Ser Trp Val Lys Ser		
	100	105	110
30	Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser Ser His Ser Tyr Gln		
	115	120	125
	Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe Arg Tyr Leu Leu Thr		
	130	135	140
	Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile Lys Ser Leu Asn Trp		
35	145	150	155
			160

[illegible]

```
<210> 5
<211> 112
<212> PRT
<213> Homo sapiens
```

<400> 5

Met	Gly	Ser	Arg	Leu	Ser	Gln	Pro	Phe	Glu	Ser	Tyr	Ile	Thr	Ala	Pro
1				5					10					15	
Pro	Gly	Thr	Ala	Ala	Ala	Pro	Ala	Lys	Pro	Ala	Pro	Pro	Ala	Thr	Pro
				20				25					30		
Gly	Ala	Pro	Thr	Ser	Pro	Ala	Glu	His	Arg	Leu	Leu	Lys	Thr	Cys	Trp
				35			40					45			
Ser	Cys	Arg	Val	Leu	Ser	Gly	Leu	Gly	Leu	Met	Gly	Ala	Gly	Gly	Tyr
				50			55				60				
Val	Tyr	Trp	Val	Ala	Arg	Lys	Pro	Met	Lys	Met	Gly	Tyr	Pro	Pro	Ser
65					70					75					80
Pro	Trp	Thr	Ile	Thr	Gln	Met	Val	Ile	Gly	Leu	Ser	Ile	Ala	Thr	Trp
				85					90					95	
Gly	Ile	Val	Val	Met	Ala	Asp	Pro	Lys	Gly	Lys	Ala	Tyr	Arg	Val	Val
				100				105					110		

6/177

<210> 6

<211> 146

<212> PRT

5 <213> Homo sapiens

<400> 6

Met Leu Ala Gly Ala Gly Arg Pro Gly Leu Pro Gln Gly Arg His Leu
1 5 10 15
10 Cys Trp Leu Leu Cys Ala Phe Thr Leu Lys Leu Cys Gln Ala Glu Ala
20 25 30
Pro Val Gln Glu Glu Lys Leu Ser Ala Ser Thr Ser Asn Leu Pro Cys
35 40 45
Trp Leu Val Glu Glu Phe Val Val Ala Glu Glu Cys Ser Pro Cys Ser
15 50 55 60
Asn Phe Arg Ala Lys Thr Thr Pro Glu Cys Gly Pro Thr Gly Tyr Val
65 70 75 80
Glu Lys Ile Thr Cys Ser Ser Ser Lys Arg Asn Glu Phe Lys Ser Cys
85 90 95
20 Arg Ser Ala Leu Met Glu Gln Arg Leu Phe Trp Lys Phe Glu Gly Ala
100 105 110
Val Val Cys Val Ala Leu Ile Phe Ala Cys Leu Val Ile Ile Arg Gln
115 120 125
Arg Gln Leu Asp Arg Lys Ala Leu Glu Lys Val Arg Lys Gln Ile Glu
25 130 135 140
Ser Ile
145

<210> 7

30 <211> 344

<212> PRT

<213> Homo sapiens

<400> 7

35 Met Asp Phe Leu Val Leu Phe Leu Phe Tyr Leu Ala Ser Val Leu Met

7/177

	1	5	10	15
	Gly	Leu	Val	Leu
	Ile	Cys	Val	Cys
	Ser	Lys	Thr	His
	Ser	Leu	Lys	Gly
	20	25	30	
	Leu	Ala	Arg	Gly
	Gly	Ala	Gln	Ile
	Phe	Ser	Cys	Ile
	Ile	Pro	Glu	Cys
5	35	40	45	
	Leu	Gln	Arg	Ala
	Val	His	Gly	Leu
	Leu	His	Tyr	Leu
	Phe	His	Thr	Arg
	50	55	60	
	Asn	His	Thr	Phe
	Ile	Val	Leu	His
	Leu	Val	Leu	Gln
	Gly	Met	Val	Tyr
	65	70	75	80
10	Thr	Glu	Tyr	Thr
	Trp	Glu	Val	Phe
	Gly	Tyr	Cys	Gln
	Glu	Leu	Glu	Leu
	85	90	95	
	Ser	Leu	His	Tyr
	Leu	Leu	Leu	Pro
	Tyr	Leu	Leu	Gly
	Val	Asn	Leu	
	100	105	110	
	Phe	Phe	Phe	Thr
	Leu	Thr	Cys	Gly
	Thr	Asn	Pro	Gly
	Ile	Ile	Thr	Lys
15	115	120	125	
	Ala	Asn	Glu	Leu
	Leu	Phe	Leu	His
	Val	Tyr	Glu	Phe
	Asp	Glu	Val	Met
	130	135	140	
	Phe	Pro	Lys	Asn
	Val	Arg	Cys	Ser
	Thr	Cys	Asp	Leu
	Arg	Lys	Pro	Ala
	145	150	155	160
20	Arg	Ser	Lys	His
	Cys	Ser	Val	Cys
	Asn	Trp	Cys	Val
	His	Arg	Phe	Asp
	165	170	175	
	His	His	Cys	Val
	Trp	Val	Asn	Asn
	Cys	Ile	Gly	Ala
	Trp	Asn	Ile	Arg
	180	185	190	
	Tyr	Phe	Leu	Ile
	Tyr	Val	Leu	Thr
	Leu	Thr	Ala	Ser
	Ala	Ala	Thr	Val
25	195	200	205	
	Ala	Ile	Val	Ser
	Thr	Thr	Phe	Leu
	Val	His	Leu	Val
	Val	Met	Ser	Asp
	210	215	220	
	Leu	Tyr	Gln	Glu
	Thr	Tyr	Ile	Asp
	Asp	Leu	Gly	His
	Leu	His	Val	Met
	225	230	235	240
30	Asp	Thr	Val	Phe
	Leu	Ile	Gln	Tyr
	Leu	Phe	Leu	Thr
	Phe	Pro	Arg	Ile
	245	250	255	
	Val	Phe	Met	Leu
	Gly	Phe	Val	Val
	Val	Leu	Ser	Phe
	Leu	Leu	Gly	Gly
	260	265	270	
	Tyr	Leu	Leu	Phe
	Val	Leu	Tyr	Leu
	Ala	Ala	Thr	Asn
	Gln	Thr	Thr	Asn
35	275	280	285	

8/177

Glu Trp Tyr Arg Gly Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val
 290 295 300
 Ala Trp Pro Pro Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser
 305 310 315 320
 5 His Gly Leu Arg Ser Asn Leu Gln Glu Ile Phe Leu Pro Ala Phe Pro
 325 330 335
 Cys His Glu Arg Lys Lys Gln Glu
 340

10 <210> 8
 <211> 97
 <212> PRT
 <213> Homo sapiens

15 <400> 8
 Met Thr Lys Lys Lys Arg Glu Asn Leu Gly Val Ala Leu Glu Ile Asp
 1 5 10 15
 Gly Leu Glu Glu Lys Leu Ser Gln Cys Arg Arg Asp Leu Glu Ala Val
 20 25 30
 20 Asn Ser Arg Leu His Ser Arg Glu Leu Ser Pro Glu Ala Arg Arg Ser
 35 40 45
 Leu Glu Lys Glu Lys Asn Ser Leu Met Asn Lys Ala Ser Asn Tyr Glu
 50 55 60
 Lys Glu Leu Lys Phe Leu Arg Gln Glu Asn Arg Lys Asn Met Leu Leu
 25 65 70 75 80
 Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala Tyr Trp Thr
 85 90 95
 Met

30 <210> 9
 <211> 124
 <212> PRT
 <213> Homo sapiens

35 <400> 9

9/177

Met Ala Thr Ser Ser Met Ser Lys Gly Cys Phe Val Phe Lys Pro Asn
 1 5 10 15
 Ser Lys Lys Arg Lys Ile Ser Leu Pro Ile Glu Asp Tyr Phe Asn Lys
 20 25 30
 5 Gly Lys Asn Glu Pro Glu Asp Ser Lys Leu Arg Phe Glu Thr Tyr Gln
 35 40 45
 Leu Ile Trp Gln Gln Met Lys Ser Glu Asn Glu Arg Leu Gln Glu Glu
 50 55 60
 Leu Asn Lys Asn Leu Phe Asp Asn Leu Ile Glu Phe Leu Gln Lys Ser
 10 65 70 75 80
 His Ser Gly Phe Gln Lys Asn Ser Arg Asp Leu Gly Gly Gln Ile Lys
 85 90 95
 Leu Arg Glu Ile Pro Thr Ala Ala Leu Val Leu Gly Ile Tyr Ala Tyr
 100 105 110
 15 Val Cys Ser Cys Met His Leu Cys Val Phe Arg Phe
 115 120

<210> 10

<211> 327

20 <212> PRT

<213> Homo sapiens

<400> 10

Met Ala Glu Leu Pro Gly Pro Phe Leu Cys Gly Ala Leu Leu Gly Phe
 25 1 5 10 15
 Leu Cys Leu Ser Gly Leu Ala Val Glu Val Lys Val Pro Thr Glu Pro
 20 25 30
 Leu Ser Thr Pro Leu Gly Lys Thr Ala Glu Leu Thr Cys Thr Tyr Ser
 35 40 45
 30 Thr Ser Val Gly Asp Ser Phe Ala Leu Glu Trp Ser Phe Val Gln Pro
 50 55 60
 Gly Lys Pro Ile Ser Glu Ser His Pro Ile Leu Tyr Phe Thr Asn Gly
 65 70 75 80
 His Leu Tyr Pro Thr Gly Ser Lys Ser Lys Arg Val Ser Leu Leu Gln
 35 85 90 95

10/177

Asn Pro Pro Thr Val Gly Val Ala Thr Leu Lys Leu Thr Asp Val His
100 105 110
Pro Ser Asp Thr Gly Thr Tyr Leu Cys Gln Val Asn Asn Pro Pro Asp
115 120 125
5 Phe Tyr Thr Asn Gly Leu Gly Leu Ile Asn Leu Thr Val Leu Val Pro
130 135 140
Pro Ser Asn Pro Leu Cys Ser Gln Ser Gly Gln Thr Ser Val Gly Gly
145 150 155 160
Ser Thr Ala Leu Arg Cys Ser Ser Ser Glu Gly Ala Pro Lys Pro Val
10 165 170 175
Tyr Asn Trp Val Arg Leu Gly Thr Phe Pro Thr Pro Ser Pro Gly Ser
180 185 190
Met Val Gln Asp Glu Val Ser Gly Gln Leu Ile Leu Thr Asn Leu Ser
195 200 205
15 Leu Thr Ser Ser Gly Thr Tyr Arg Cys Val Ala Thr Asn Gln Met Gly
210 215 220
Ser Ala Ser Cys Glu Leu Thr Leu Ser Val Thr Glu Pro Ser Gln Gly
225 230 235 240
Arg Val Ala Gly Ala Leu Ile Gly Val Leu Leu Gly Val Leu Leu Leu
20 245 250 255
Ser Val Ala Ala Phe Cys Leu Val Arg Phe Gln Lys Glu Arg Gly Lys
260 265 270
Lys Pro Lys Glu Thr Tyr Gly Gly Ser Asp Leu Arg Glu Asp Ala Ile
275 280 285
25 Ala Pro Gly Ile Ser Glu His Thr Cys Met Arg Ala Asp Ser Ser Lys
290 295 300
Gly Phe Leu Glu Arg Pro Ser Ser Ala Ser Thr Val Thr Thr Thr Lys
305 310 315 320
Ser Lys Leu Pro Met Val Val
30 325

<210> 11

<211> 375

<212> DNA

35 <213> Homo sapiens

11/177

<400> 11

atggccaagt acctggccca gatcattgtg atgggcgtgc aggtggtggg cagggccttt 60
gcacgggcct tgcggcagga gtttgcagcc agccggggccg cagctgatgc ccgaggacgc 120
5 gctggacacc ggtctgcage cgcttccaac ctctccggcc tcagcctcca ggaggcacag 180
cagattctca acgtgtccaa gctgagccct gaggaggtec agaagaacta tgaacactta 240
tttaaggtga atgataaata cgtgggtggc tcctttctacc tgcagtcaaa ggtgggtccgc 300
gcaaaggagc gcctggatga ggaactcaaa atccaggccc aggaggacag agaaaaaggg 360
cagatgcccc atacg 375

10

<210> 12

<211> 393

<212> DNA

<213> Homo sapiens

15

<400> 12

atggcaggca tcaaagcttt gattagtttg tcctttggag gagcaatcgg actgatgttt 60
ttgatgcttg gatgtgccct tccaatatac aacaaatact ggccctctct tgttctatct 120
ttttacatcc tttcacctat tccatactgc atagcaagaa gattagtgga tgatacagat 180
20 gctatgagta acgcttgtaa ggaacttgcc atctttctta caacggggcat tgcgtgtca 240
gettttggac tccctattgt atttgccaga gcacatctga ttgagtgggg agcttgtgca 300
cttgttctca caggaaacac agtcactctt gcaactatac taggcttttt cttggtcttt 360
ggaagcaatg acgacttcag ctggcagcag tgg 393

25

<210> 13

<211> 726

<212> DNA

<213> Homo sapiens

30

<400> 13

atggcgaagc acgagcagat cctggtctct gatccgccc cagacctcaa attcaaaggc 60
cccttcacag atgtagtcac tacaaatctt aaattgcgaa atccatcgga tagaaaagtg 120
tgtttcaaag tgaagactac agcacctcgc cggtagctgt tgaggcccaa cagtgggaatt 180
attgacctag ggtcaactgt gactgtttca gtaatgtac agccctttga ctatgatccg 240
35 aatgaaaaga gtaaacacaa gtttatggta cagacaattt ttgctccacc aaacacttca 300

12/177

	gatatggaag ctgtgtggaa agaggcaaaa cctgatgaat taatggattc caaattgaga	360
	tgcgatatttg aaatgcccaa tgaaaatgat aaattgaatg atatggaacc tagcaaagct	420
	gttccactga atgcatctaa gcaagatgga cctatgccaa aaccacacag tgtttcactt	480
	aatgataccg aaacaaggaa actaatggaa gagtgtaaaa gacttcaggg agaaatgatg	540
5	aagctatcag aagaaaatcg gcacctgaga gatgaagggt taaggctcag aaaggtagca	600
	cattcggata aacctggatc aacctcaact gcatecttca gagataatgt caccagtcct	660
	cttccttcac ttcttgttgt aattgcagcc attttcattg gattttttct agggaaatc	720
	atcttg	726
10	<210> 14	
	<211> 792	
	<212> DNA	
	<213> Homo sapiens	
15	<400> 14	
	atgttcgttc cctgcgggga gtcggceccc gacettgccg gettcaccct cctaatagcca	60
	gcagtatctg ttggaaatgt tggccagctt gcaatggatc tgattatttc tacactgaat	120
	atgtctaaga ttggttactt ctataccgat tgtcttgtgc caatggttgg aaacaatcca	180
	tatgcgacca cagaaggaaa ttcaacagaa cttagcataa atgctgaaat gtattcattg	240
20	cettcaagaa agctggtggc tctacagtta agatccattt ttattaagta taaatcaaag	300
	ccattctgtg aaaaaactgct ttccctgggtg aaaagcagtg gctgtgccag agtcattgtt	360
	ctttcgagca gtcattcata tcagcgtaat gatctgcagc ttcgtagtac tcccttccgg	420
	tacctactta caccttccat gcaaaaaagt gttcaaaata aaataaagag cottaactgg	480
	gaagaaatgg aaaaaagccg gtgcattcct gaaatagatg attccgagtt ttgtatccgc	540
25	attccgggag gaggtatcac aaaaacactc tatgatgaaa gctgttctaa agaaatccaa	600
	atggcagttc tgctgaaatt tgtttcagaa ggggacaaca tcccagatgc attaggtctt	660
	gttgagtatc ttaatgagtg gcttcagata ctcaaaccac ttagcgatga cccacagta	720
	tctgcctcac ggtggaaaat accaagttct tggagattac tctttggcag tgggtcttccc	780
	cctgcacttt tc	792
30	<210> 15	
	<211> 336	
	<212> DNA	
	<213> Homo sapiens	
35		

13/177

<400> 15

atgggggtctc ggttggtccca gccttttgag tcctatatca ctgcgcctcc cgggtaccgcc 60
 gccgcgccccg ccaaacctgc gccccagct acaccggag cgcgcacctc ccagcagaa 120
 caccgcctgt tgaagacctg ctggagctgt cgcgtgcttt ctgggttggg gctgatggg 180
 5 gcgggcgggt acgtgtactg ggtggcacgg aagcccatga agatgggata cccccgagt 240
 ccatggacca ttacgcagat ggtcatcggc ctacgcattg ccacctgggg tctcgttgtc 300
 atggcagacc ccaaaggga ggcctaccgc gttgtt 336

<210> 16

10 <211> 438

<212> DNA

<213> Homo sapiens

<400> 16

15 atgcttgagg gtgccgggag gcctggcctc cccaggggc gccacctctg ctggttctc 60
 tgtgctttca ccttaaagct ctgccaaagca gaggtctccg tgcaggaaga gaagctgtca 120
 gcaagcacct caaatttgcc atgctggctg gtggaagagt ttgtggtagc agaagagtgc 180
 tctccatgct ctaatttccg ggctaaaact acccctgagt gtggtccac aggatatgta 240
 gagaaaatca catgcagctc atctaagaga aatgagttca aaagctgccg ctacgctttg 300
 20 atggaacaac gcttattttg gaagttcgaa ggggctgtcg tgtgtgtggc cctgatcttc 360
 gcttgctcttgc tcatcattcg tcagcgacaa ttggacagaa aggcctctgga aaaggtccgg 420
 aagcaaatcg agtccata 438

<210> 17

25 <211> 1032

<212> DNA

<213> Homo sapiens

<400> 17

30 atggactttc tggctctctt cttgttctac ctggtctcgg tgcctgatggg tcttgttctt 60
 atctgcgtct gctcgaaaac ccatagcttg aaaggcctgg ccaggggagg agcacagata 120
 ttttctgtga taattccaga atgtcttcag agagccgtgc atggattgct tcattacctt 180
 ttccatacga gaaaccacac cttcattgtc ctgcacctgg tcttgcaagg gatggtttat 240
 actgagtaca cctgggaagt atttggttac tgtcaggagc tggagttgtc cttgcattac 300
 35 cttctttctgc cctatctgct gctaggtgta aacctgtttt ttttcacctt gacttggtga 360

14/177

	accaatcctg gcattataac aaaagcaa at gaattattat ttcttcatgt ttatgaattt	420
	gatgaagtga tgtttccaaa gaacgtgagg tgctctactt gtgatttaag gaaaccagct	480
	cgatccaagc actgcagtgt gtgtaactgg tgtgtgcacc gtttcgacca tcaactgtgtt	540
	tgggtgaaca actgcacggg ggccctggaac atcaggtact tcctcatcta cgtcttgacc	600
5	ttgacggcct cggctgccac cgtcgccatt gtgagcacca cttttctggt ccacttggtg	660
	gtgatgtcag atttatacca ggagacttac atcgatgacc ttggacacct ccattgttatg	720
	gacacggctt ttcttattca gtacctgttc ctgacttttc caccggattgt ctccatgctg	780
	ggctttgtcg tggttctgag ctccctcctg ggtggetacc tgttggttgt cctgtatctg	840
	gcggccacca accagactac taacgagtgg tacagaggtg actgggcctg gtgccagcgt	900
10	tgcccccttg tggcctggcc tccgtcagca gagccccaag tccaccggaa cattcactcc	960
	catgggcttc ggagcaacct tcaagagatc tttctacctg cctttccatg tcatgagagg	1020
	aagaaacaag aa	1032
	<210> 18	
15	<211> 291	
	<212> DNA	
	<213> Homo sapiens	
	<400> 18	
20	atgactaaaa agaagcggga gaatctgggc gtcgctctag agatcgatgg gctagaggag	60
	aagctgtccc agtgctggag agacctggag gccgtgaact ccagactcca cagccgggag	120
	ctgagcccag aggccaggag gtcctctggag aaggagaaaa acagccta at gaacaaagcc	180
	tccaactacg agaaggaact gaagtttctt cggcaagaga accggaagaa catgctgctc	240
	tctgtggcca tctttatcct cctgacgctc gtctatgcct actggaccat g	291
25	<210> 19	
	<211> 372	
	<212> DNA	
	<213> Homo sapiens	
30	<400> 19	
	atggctacgt cctcgatgtc taagggttgc tttgttttta agccaaactc caaaaagaga	60
	aagatctctc tgccaataga ggactatctt aacaaaggga aaaatgagcc tgaggacagt	120
	aagcttcgat tcgaaaactta tcagttgata tggcagcaga tgaaatctga aaatgagcga	180
35	ctacaagagg aattaaataa aaacttgttt gacaatctga ttgaatttct gcaaaaatca	240

15/177

	cattctggat tccagaagaa ttcaagagac ttgggcggtc aaataaaact cagagaaatt	300
	ccaactgctg ctcttgttct tggatatatat gcgtatgtt gttcatgcat gcctctctgt	360
	gtatttcgtt tt	372
5	<210> 20	
	<211> 981	
	<212> DNA	
	<213> Homo sapiens	
10	<400> 20	
	atggccgagc tcccggggcc ctttctctgc ggggccctgc taggttctct gtgectgagt	60
	gggctggccg tggaggtgaa ggtacccaca gagccgctga gcacgccctt ggggaagaca	120
	gccgagctga cctgcaccta cagcacgtcg gtgggagaca gcttcgccct ggagtgaggc	180
	tttgtgcagc ctgggaaacc catctctgag tcccatccaa tctgtactt caccaatggc	240
15	catctgtatc caactggttc taagtcaaag cgggtcagcc tgcctcagaa cccccccaca	300
	gtgggggttg ccacactgaa actgactgac gtccaccctt cagatactgg aacctacctc	360
	tgccaaagtc acaaccacc agattttctac accaatgggt tggggctaata caaccttact	420
	gtgctggttc cccccagtaa tcccttatgc agtcagagtg gacaaacctc tgtgggaggc	480
	tctactgcac tgagatgcag ctcttccgag ggggtccta agccagtgtg caactgggtg	540
20	cgtcttgga cttttctctac accttctctt ggcagcatgg ttcaagatga ggtgtctggc	600
	cagctcatte tcaccaacct ctccctgacc tctcgggca cctaccgctg tgtggccacc	660
	aaccagatgg gcagtgcatc ctgtgagctg acctctctg tgaccgaacc ctcccaaggc	720
	cgagtggccg gagctctgat tggggtgctc ctgggcgtgc tgttgcgtgc agttgctgcg	780
	ttctgcctgg tcaggttcca gaaagagagg gggaagaagc ccaaggagac atatgggggt	840
25	agtgaccttc gggaggatgc catcgtctct gggatctctg agcacacttg tatgagggt	900
	gattctagca aggggttctt ggaaagacct tcgtctgcca gcaccgtgac gaccaccaag	960
	tccaagctcc ctatggctgt g	981
	<210> 21	
30	<211> 510	
	<212> DNA	
	<213> Homo sapiens	
	<220>	
	<221> CDS	
35	<222> (66)...(443)	

16/177

<400> 21

acgcttgatc cccggccgcg gggccaggaa gtcggagttt gagccccgga ggcagagcgg 60

ctgcc atg gcc aag tac ctg gcc cag atc att gtg atg ggc gtg cag gtg 110

5 Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met Gly Val Gln Val

1 5 10 15

gtg ggc agg gcc ttt gca cgg gcc ttg cgg cag gag ttt gca gcc agc 158

Val Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu Phe Ala Ala Ser

20 25 30

10 cgg gcc gca gct gat gcc cga gga cgc gct gga cac cgg tct gca gcc 206

Arg Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala

35 40 45

gct tcc aac ctc tcc ggc ctc agc ctc cag gag gca cag cag att ctc 254

Ala Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu

15 50 55 60

aac gtg tcc aag ctg agc cct gag gag gtc cag aag aac tat gaa cac 302

Asn Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys Asn Tyr Glu His

65 70 75

tta ttt aag gtg aat gat aaa tcc gtg ggt ggc tcc ttc tac ctg cag 350

20 Leu Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln

80 85 90 95

tca aag gtg gtc cgc gca aag gag cgc ctg gat gag gaa ctc aaa atc 398

Ser Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile

100 105 110

25 cag gcc cag gag gac aga gaa aaa ggg cag atg ccc cat acg tgactgctc 450

Gln Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His Thr

115 120 125

gtcccccccg cccacccgcg cgctctaat ttatagcttg gtaataaatt tcttttctgc 510

30 <210> 22

<211> 697

<212> DNA

<213> Homo sapiens

<220>

35 <221> CDS

17/177

<222> (104)...(499)

<400> 22

	acttcggggt gttgtctggc cgccgtagcg cgtcttgggt ctcccggtg ccgctgctgc	60
5	cgccgcccgc tcgggtcgtg gagccaggag cgacgtcacc gcc atg gca ggc atc	115
	Met Ala Gly Ile	
	1	
	aaa gct ttg att agt ttg tcc ttt gga gga gca atc gga ctg atg ttt	163
	Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala Ile Gly Leu Met Phe	
10	5 10 15 20	
	ttg atg ctt gga tgt gcc ctt cca ata tac aac aaa tac tgg ccc ctc	211
	Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr Asn Lys Tyr Trp Pro Leu	
	25 30 35	
	ttt gtt cta ttt ttt tac atc ctt tca cct att cca tac tgc ata gca	259
15	Phe Val Leu Phe Phe Tyr Ile Leu Ser Pro Ile Pro Tyr Cys Ile Ala	
	40 45 50	
	aga aga tta gtg gat gat aca gat gct atg agt aac gct tgt aag gaa	307
	Arg Arg Leu Val Asp Asp Thr Asp Ala Met Ser Asn Ala Cys Lys Glu	
	55 60 65	
20	ctt gcc atc ttt ctt aca acg ggc att gtc gtg tca gct ttt gga ctc	355
	Leu Ala Ile Phe Leu Thr Thr Gly Ile Val Val Ser Ala Phe Gly Leu	
	70 75 80	
	cct att gta ttt gcc aga gca cat ctg att gag tgg gga gct tgt gca	403
	Pro Ile Val Phe Ala Arg Ala His Leu Ile Glu Trp Gly Ala Cys Ala	
25	85 90 95 100	
	ctt gtt ctc aca gga aac aca gtc atc ttt gca act ata cta ggc ttt	451
	Leu Val Leu Thr Gly Asn Thr Val Ile Phe Ala Thr Ile Leu Gly Phe	
	105 110 115	
	ttc ttg gtc ttt gga agc aat gac gac ttc agc tgg cag cag tgg tgaa	500
30	Phe Leu Val Phe Gly Ser Asn Asp Asp Phe Ser Trp Gln Gln Trp	
	120 125 130	
	aagaaattac tgaactattg tcaaattggac ttctgtcat ttgttgcca ttcacgcaca	560
	caggagatgg ggcagttaat gctgaatggg atagcaagcc tcttgggggg atttttaggtg	620
	ctcccttctc acttttattg taagcatact attttcacag agacttgetg aaggattaaa	680
35	aggattttct cttttgg	697

18/177

<210> 23
 <211> 1619
 <212> DNA
 5 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (287)...(1015)

10 <400> 23
 gcagaggccg tcacgtgggt cgcgcgagget cgcaagtgcg cgtggccgtg gcggttggtg 60
 tgggggttgag tcagttgtgg gacccggagc tgetgaccca gcgggtggcc caccgaaccg 120
 gtgacacagc ggcaggcggt agggctcggg agccgcgagc ctggcctcgt cctagagetc 180
 ggccgagccg tcgccgccgt cgtcccccgc cccagtcag caaacgcgcg ccgcgggcgc 240
 15 gccccgcctc tgcgtgtgt ctcgatggc gtccgcctca ggggcc atg gcg aag 295
 Met Ala Lys
 1
 cac gag cag atc ctg gtc ctc gat ccg ccc aca gac ctc aaa ttc aaa 343
 His Glu Gln Ile Leu Val Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys
 20 5 10 15
 ggc ccc ttc aca gat gta gtc act aca aat ctt aaa ttg cga aat cca 391
 Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu Lys Leu Arg Asn Pro
 20 25 30 35
 tcg gat aga aaa gtg tgt ttc aaa gtg aag act aca gca cct cgc cgg 439
 25 Ser Asp Arg Lys Val Cys Phe Lys Val Lys Thr Thr Ala Pro Arg Arg
 40 45 50
 tac tgt gtg agg ccc aac agt gga att att gac cca ggg tca act gtg 487
 Tyr Cys Val Arg Pro Asn Ser Gly Ile Ile Asp Pro Gly Ser Thr Val
 55 60 65
 30 act gtt tca gta atg cta cag ccc ttt gac tat gat ccg aat gaa aag 535
 Thr Val Ser Val Met Leu Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys
 70 75 80
 agt aaa cac aag ttt atg gta cag aca att ttt gct cca cca aac act 583
 Ser Lys His Lys Phe Met Val Gln Thr Ile Phe Ala Pro Pro Asn Thr
 35 85 90 95

19/177

	tca gat atg gaa gct gtg tgg aaa gag gca aaa cct gat gaa tta atg	631
	Ser Asp Met Glu Ala Val Trp Lys Glu Ala Lys Pro Asp Glu Leu Met	
	100 105 110 115	
	gat tcc aaa ttg aga tgc gta ttt gaa atg ccc aat gaa aat gat aaa	679
5	Asp Ser Lys Leu Arg Cys Val Phe Glu Met Pro Asn Glu Asn Asp Lys	
	120 125 130	
	ttg aat gat atg gaa cct agc aaa gct gtt cca ctg aat gca tct aag	727
	Leu Asn Asp Met Glu Pro Ser Lys Ala Val Pro Leu Asn Ala Ser Lys	
	135 140 145	
10	caa gat gga cct atg cca aaa cca cac agt gtt tca ctt aat gat acc	775
	Gln Asp Gly Pro Met Pro Lys Pro His Ser Val Ser Leu Asn Asp Thr	
	150 155 160	
	gaa aca agg aaa cta atg gaa gag tgt aaa aga ctt cag gga gaa atg	823
	Glu Thr Arg Lys Leu Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Met	
15	165 170 175	
	atg aag cta tca gaa gaa aat cgg cac ctg aga gat gaa ggt tta agg	871
	Met Lys Leu Ser Glu Glu Asn Arg His Leu Arg Asp Glu Gly Leu Arg	
	180 185 190 195	
	ctc aga aag gta gca cat tcg gat aaa cct gga tca acc tca act gca	919
20	Leu Arg Lys Val Ala His Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala	
	200 205 210	
	tcc ttc aga gat aat gtc acc agt cct ctt cct tca ctt ctt gtt gta	967
	Ser Phe Arg Asp Asn Val Thr Ser Pro Leu Pro Ser Leu Leu Val Val	
	215 220 225	
25	att gca gcc att ttc att gga ttc ttt cta ggg aaa ttc atc ttg	1012
	Ile Ala Ala Ile Phe Ile Gly Phe Phe Leu Gly Lys Phe Ile Leu	
	230 235 240	
	tagagtgaag catgcagagt gctgtttctt tttttttttt ttctcttgac cagaaaaa	1070
	gatttgttta cctaccattt cattggtagt atggcccacg gtgaccattt ttttgtgtgt	1130
30	acagcgtcat ataggttttg cctttaatga tctcttacgg ttagaaaaca caataaaaac	1190
	aaactgttcg gctactggac aggttgata ttaccagatc atcactagca gatgtcagtt	1250
	gcacattgag tcctttatga aattcataaa taaagaattg ttctttcttt gtgggtttta	1310
	taagagttca agaattgttc agagtcttgt aaatgttatt ttaataatcc ctttaaattt	1370
	tatctgttgc tgttacctet tgaaatatga tttatttaga ttgctaatacc cactcattca	1430
35	ggaaatgccca agaggtattc cttggggaaa tgggtgcctet tacagtgtaa atttttctc	1490

20/177

ctttaccttt gctaatatca tggcagaatt tttcttatcc cttgtgaggc agttgttgac 1550
 tgagtttttc atccttaciaa tcctgtccca tgggtatttaa cataaaaaaa aataaaaactg 1610
 ttaacagat 1619

5 <210> 24
 <211> 1066
 <212> DNA
 <213> Homo sapiens
 <220>
 10 <221> CDS
 <222> (65)...(859)

<400> 24
 cttcttgctg ccctcggttct tgccggggcc gcggttagtc cctgctggcc accccactgc 60
 15 gacc atg ttc gtt ccc tgc ggg gag tgc gcc ccc gac ctt gcc ggc ttc 109
 Met Phe Val Pro Cys Gly Glu Ser Ala Pro Asp Leu Ala Gly Phe
 1 5 10 15
 acc ctc cta atg cca gca gta tct gtt gga aat gtt ggc cag ctt gca 157
 Thr Leu Leu Met Pro Ala Val Ser Val Gly Asn Val Gly Gln Leu Ala
 20 20 25 30
 atg gat ctg att att tct aca ctg aat atg tct aag att ggt tac ttc 205
 Met Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys Ile Gly Tyr Phe
 35 40 45
 tat acc gat tgt ctt gtg cca atg gtt gga aac aat cca tat gcg acc 253
 25 Tyr Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn Pro Tyr Ala Thr
 50 55 60
 aca gaa gga aat tca aca gaa ctt agc ata aat gct gaa gtg tat tca 301
 Thr Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala Glu Val Tyr Ser
 65 70 75
 30 ttg cct tca aga aag ctg gtg gct cta cag tta aga tcc att ttt att 349
 Leu Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg Ser Ile Phe Ile
 80 85 90 95
 aag tat aaa tca aag cca ttc tgt gaa aaa ctg ctt tcc tgg gtg aaa 397
 Lys Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu Ser Trp Val Lys
 35 100 105 110

21/177

	agc agt ggc tgt gcc aga gtc att gtt ctt tcg agc agt cat tca tat	445
	Ser Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser Ser His Ser Tyr	
	115 120 125	
5	cag cgt aat gat ctg cag ctt cgt agt act ccc ttc cgg tac cta ctt	493
	Gln Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe Arg Tyr Leu Leu	
	130 135 140	
	aca cct tcc atg caa aaa agt gtt caa aat aaa ata aag agc ctt aac	541
	Thr Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile Lys Ser Leu Asn	
	145 150 155	
10	tgg gaa gaa atg gaa aaa agc cgg tgc att cct gaa ata gat gat tcc	589
	Trp Glu Glu Met Glu Lys Ser Arg Cys Ile Pro Glu Ile Asp Asp Ser	
	160 165 170 175	
	gag ttt tgt atc cgc att ccg gga gga ggt atc aca aaa aca ctc tat	637
	Glu Phe Cys Ile Arg Ile Pro Gly Gly Gly Ile Thr Lys Thr Leu Tyr	
15	180 185 190	
	gat gaa agc tgt tct aaa gaa atc caa atg gca gtt ctg ctg aaa ttt	685
	Asp Glu Ser Cys Ser Lys Glu Ile Gln Met Ala Val Leu Leu Lys Phe	
	195 200 205	
20	gtt tca gaa ggg gac aac atc cca gat gca tta ggt ctt gtt gag tat	733
	Val Ser Glu Gly Asp Asn Ile Pro Asp Ala Leu Gly Leu Val Glu Tyr	
	210 215 220	
	ctt aat gag tgg ctt cag ata ctc aaa cca ctt agc gat gac ccc aca	781
	Leu Asn Glu Trp Leu Gln Ile Leu Lys Pro Leu Ser Asp Asp Pro Thr	
	225 230 235	
25	gta tct gcc tca cgg tgg aaa ata cca agt tct tgg aga tta ctc ttt	829
	Val Ser Ala Ser Arg Trp Lys Ile Pro Ser Ser Trp Arg Leu Leu Phe	
	240 245 250 255	
	ggc agt ggt ctt ccc cct gca ctt ttc tgatctaatt tctgttttat acct	880
	Gly Ser Gly Leu Pro Pro Ala Leu Phe	
30	260	
	tatacccaaaa acacttacta ccaacacagc tgtaaacaat tctatacaaaa aaaattgtat	940
	gatctggtat taggaaatta ctttcacagt aaatatcaaaa gaaaaaagat taagggtctc	1000
	tttgccatgc ttttcatcat atgcaccaaaa tgtaaatttt gtacaataaaa attttatttc	1060
	ctaagt	1066
35		

22/177

<211> 618

<213> Homo sapiens

<220>

<222> (54)...(392)

10 gtttacgcc a gtttgaacca aagacgcccc aggttgaggc cgagttccag agc atg 56
Met

15	5	10	15	
ggt acc gcc gcc gcg ccc gcc aaa cct gcg ccc cca gct aca ccc gga				152
Gly Thr Ala Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro Gly				
	20	25	30	

tgt cgc gtg ctt tct ggg ttg ggg ctg atg ggg gcg ggc ggg tac gtg 248
Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr Val
50 55 60 65

tgg acc att acg cag atg gtc atc ggc ctc agc att gcc acc tgg ggt 344
Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Ile Ala Thr Trp Gly

100	105	110	
gaaagtacca ccagtgaatc tgtcttctgt ctctgtccct ttccccgtga cacacacagc 450			
aggcatggaa tttaatgggt gttctggaca gacacttgta catggacaga catcactact 510			

23/177

	gtggatacta caagactgag aagaaaatcg tatgttgta ttctctggct atggagtgtt	570
	tgtggccttc acagatttca caggaaccaa taaatccctc agagaagt	618
	<210> 26	
5	<211> 1021	
	<212> DNA	
	<213> Homo sapiens	
	<220>	
	<221> CDS	
10	<222> (413)...(853)	
	<400> 26	
	aagactataa gccccagcgg gcgacgaccg aacgccccg ggaacacagg gccccgagct	60
	cggccccgg cccgaggatc ctccacgggg ctagatggct gcgtcggggg cgggagcggg	120
15	ggtgagcggg cgctagggcc gcgagcccc gccggccctt cctccagcgc cctgcggacc	180
	ccgcagaagg cgctcgctc cctagccgc aaaaacatat cgatttttct cgctgtggca	240
	acggggacgt cctgatagat cctctgctcc aataggcaac tccggccttc cctgccctga	300
	cctggaacct ctgggagggc tgcagagtaa gtgccgcctc tgcgctccga cggaggcaacg	360
	aggcctgtgg agtaggtccc tctgttccga caggtgcgac acttggeget cc atg ctt	418
20		Met Leu
		1
	gcg ggt gcc ggg agg cct ggc ctc ccc cag ggc cgc cac ctc tgc tgg	466
	Ala Gly Ala Gly Arg Pro Gly Leu Pro Gln Gly Arg His Leu Cys Trp	
	5 10 15	
25	ttg ctc tgt gct ttc acc tta aag ctc tgc caa gca gag gct ccc gtg	514
	Leu Leu Cys Ala Phe Thr Leu Lys Leu Cys Gln Ala Glu Ala Pro Val	
	20 25 30	
	cag gaa gag aag ctg tca gca agc acc tca aat ttg cca tgc tgg ctg	562
	Gln Glu Glu Lys Leu Ser Ala Ser Thr Ser Asn Leu Pro Cys Trp Leu	
30	35 40 45 50	
	gtg gaa gag ttt gtg gta gca gaa gag tgc tct cca tgc tct aat ttc	610
	Val Glu Glu Phe Val Val Ala Glu Glu Cys Ser Pro Cys Ser Asn Phe	
	55 60 65	
	cgg gct aaa act acc cct gag tgt ggt ccc aca gga tat gta gag aaa	658
35	Arg Ala Lys Thr Thr Pro Glu Cys Gly Pro Thr Gly Tyr Val Glu Lys	

24/177

	70	75	80	
	atc aca tgc agc tca tct aag aga aat gag ttc aaa agc tgc cgc tca			706
	Ile Thr Cys Ser Ser Ser Lys Arg Asn Glu Phe Lys Ser Cys Arg Ser			
	85	90	95	
5	gct ttg atg gaa caa cgc tta ttt tgg aag ttc gaa ggg gct gtc gtg			754
	Ala Leu Met Glu Gln Arg Leu Phe Trp Lys Phe Glu Gly Ala Val Val			
	100	105	110	
	tgt gtg gcc ctg atc ttc gct tgt ctt gtc atc att cgt cag cga caa			802
	Cys Val Ala Leu Ile Phe Ala Cys Leu Val Ile Ile Arg Gln Arg Gln			
10	115	120	125	130
	ttg gac aga aag gct ctg gaa aag gtc cgg aag caa atc gag tcc ata			850
	Leu Asp Arg Lys Ala Leu Glu Lys Val Arg Lys Gln Ile Glu Ser Ile			
	135	140	145	
	tagctacatt ccacccttgt atcctgggtc ttagagaccc tatctcagac agtgaaagtg			910
15	aaatggactg atttgcactc ttggttcttt ggagccttgt ggtggaatcc ccttttcccc			970
	atcttcttct ttcagatcat taatgagcag aataaaaaga gtaaatggt t			1021
	<210> 27			
	<211> 1432			
20	<212> DNA			
	<213> Homo sapiens			
	<220>			
	<221> CDS			
	<222> (331)...(1365)			
25	<400> 27			
	atcgcgcccg ggaggcgccg gagcccagcg gctggcgggc cgccgtccca cccccacctc			60
	gcccagatcc gggggcgccc cggtgtcccc tccagagctg ctgcactcca cgcccccta			120
	ccagggtccc agccccagc gaaatctccg accaggcccc cccaggagcc agatccaggc			180
30	tcttggaaga accatgtccg gcagctactg gtcattgccag gcacacactg ctgcccgaaga			240
	ggagctgctg tttgaattat ctgtgaatgt tgggaagagg aatgccagag ctgccggctg			300
	aaaattaccc aaccaagaga aatctgcagg atg gac ttt ctg gtc etc ttc ttg			354
	Met Asp Phe Leu Val Leu Phe Leu			
	1	5		
35	ttc tac ctg gct tcc gtg ctg atg ggt ctt gtt ctt atc tgc gtc tgc			402

25/177

	Phe Tyr Leu Ala Ser Val Leu Met Gly Leu Val Leu Ile Cys Val Cys	
	10 15 20	
	tgc aaa acc cat agc ttg aaa ggc ctg gcc agg gga gga gca cag ata	450
	Ser Lys Thr His Ser Leu Lys Gly Leu Ala Arg Gly Gly Ala Gln Ile	
5	25 30 35 40	
	ttt tcc tgt ata att cca gaa tgt ctt cag aga gcc gtg cat gga ttg	498
	Phe Ser Cys Ile Ile Pro Glu Cys Leu Gln Arg Ala Val His Gly Leu	
	45 50 55	
	ctt cat tac ctt ttc cat acg aga aac cac acc ttc att gtc ctg cac	546
10	Leu His Tyr Leu Phe His Thr Arg Asn His Thr Phe Ile Val Leu His	
	60 65 70	
	ctg gtc ttg caa ggg atg gtt tat act gag tac acc tgg gaa gta ttt	594
	Leu Val Leu Gln Gly Met Val Tyr Thr Glu Tyr Thr Trp Glu Val Phe	
	75 80 85	
15	ggc tac tgt cag gag ctg gag ttg tcc ttg cat tac ctt ctt ctg ccc	642
	Gly Tyr Cys Gln Glu Leu Glu Leu Ser Leu His Tyr Leu Leu Leu Pro	
	90 95 100	
	tat ctg ctg cta ggt gta aac ctg ttt ttt ttc acc ctg act tgt gga	690
	Tyr Leu Leu Leu Gly Val Asn Leu Phe Phe Phe Thr Leu Thr Cys Gly	
20	105 110 115 120	
	acc aat cct ggc att ata aca aaa gca aat gaa tta tta ttt ctt cat	738
	Thr Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu Leu Leu Phe Leu His	
	125 130 135	
	gtt tat gaa ttt gat gaa gtg atg ttt cca aag aac gtg agg tgc tct	786
25	Val Tyr Glu Phe Asp Glu Val Met Phe Pro Lys Asn Val Arg Cys Ser	
	140 145 150	
	act tgt gat tta agg aaa cca gct cga tcc aag cac tgc agt gtg tgt	834
	Thr Cys Asp Leu Arg Lys Pro Ala Arg Ser Lys His Cys Ser Val Cys	
	155 160 165	
30	aac tgg tgt gtg cac cgt ttc gac cat cac tgt gtt tgg gtg aac aac	882
	Asn Trp Cys Val His Arg Phe Asp His His Cys Val Trp Val Asn Asn	
	170 175 180	
	tgc atc ggg gcc tgg aac atc agg tac ttc ctc atc tac gtc ttg acc	930
	Cys Ile Gly Ala Trp Asn Ile Arg Tyr Phe Leu Ile Tyr Val Leu Thr	
35	185 190 195 200	

26/177

	ttg acg gcc tcg gct gcc acc gtc gcc att gtg agc acc act ttt ctg	978
	Leu Thr Ala Ser Ala Ala Thr Val Ala Ile Val Ser Thr Thr Phe Leu	
	205 210 215	
5	gtc cac ttg gtg gtg atg tca gat tta tac cag gag act tac atc gat	1026
	Val His Leu Val Val Met Ser Asp Leu Tyr Gln Glu Thr Tyr Ile Asp	
	220 225 230	
	gac ctt gga cac ctc cat gtt atg gac acg gtc ttt ctt att cag tac	1074
	Asp Leu Gly His Leu His Val Met Asp Thr Val Phe Leu Ile Gln Tyr	
	235 240 245	
10	ctg ttc ctg act ttt cca cgg att gtc ttc atg ctg ggc ttt gtc gtg	1122
	Leu Phe Leu Thr Phe Pro Arg Ile Val Phe Met Leu Gly Phe Val Val	
	250 255 260	
	GTT CTG AGC TTC CTC CTG GGT GGC TAC CTG TTG TTT GTC CTG TAT CTG	1170
	Val Leu Ser Phe Leu Leu Gly Gly Tyr Leu Leu Phe Val Leu Tyr Leu	
15	265 270 275 280	
	gcg gcc acc aac cag act act aac gag tgg tac aga ggt gac tgg gcc	1218
	Ala Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr Arg Gly Asp Trp Ala	
	285 290 295	
20	tgg tgc cag cgt tgt ccc ctt gtg gcc tgg cct ccg tca gca gag ccc	1266
	Trp Cys Gln Arg Cys Pro Leu Val Ala Trp Pro Pro Ser Ala Glu Pro	
	300 305 310	
	caa gtc cac cgg aac att cac tcc cat ggg ctt cgg agc aac ctt caa	1314
	Gln Val His Arg Asn Ile His Ser His Gly Leu Arg Ser Asn Leu Gln	
	315 320 325	
25	gag atc ttt cta cct gcc ttt cca tgt cat gag agg aag aaa caa gaa	1362
	Glu Ile Phe Leu Pro Ala Phe Pro Cys His Glu Arg Lys Lys Gln Glu	
	330 335 340	
	tgacaagtgt atgactgcct ttgagctgta gttcccggtt atttacacat gtggatcc	1420
30	tcgttttcca ag	1432
	<210> 28	
	<211> 601	
	<212> DNA	
	<213> Homo sapiens	
35	<220>	

27/177

<221> CDS

<222> (62)...(355)

<400> 28

5	atgcgcacat agcgacttgg tgggcgcgtc cagtgatgac tgggggatcc cggcaagtaa	60
	c atg act aaa aag aag cgg gag aat ctg ggc gtc gct cta gag atc gat	109
	Met Thr Lys Lys Lys Arg Glu Asn Leu Gly Val Ala Leu Glu Ile Asp	
	1 5 10 15	
	ggg cta gag gag aag ctg tcc cag tgt cgg aga gac ctg gag gcc gtg	157
10	Gly Leu Glu Glu Lys Leu Ser Gln Cys Arg Arg Asp Leu Glu Ala Val	
	20 25 30	
	aac tcc aga ctc cac agc cgg gag ctg agc cca gag gcc agg agg tcc	205
	Asn Ser Arg Leu His Ser Arg Glu Leu Ser Pro Glu Ala Arg Arg Ser	
	35 40 45	
15	ctg gag aag gag aaa aac agc cta atg aac aaa gcc tcc aac tac gag	253
	Leu Glu Lys Glu Lys Asn Ser Leu Met Asn Lys Ala Ser Asn Tyr Glu	
	50 55 60	
	aag gaa ctg aag ttt ctt cgg caa gag aac cgg aag aac atg ctg ctc	301
	Lys Glu Leu Lys Phe Leu Arg Gln Glu Asn Arg Lys Asn Met Leu Leu	
20	65 70 75 80	
	tct gtg gcc atc ttt atc ctc ctg acg ctc gtc tat gcc tac tgg acc	349
	Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala Tyr Trp Thr	
	85 90 95	
	atg tgagcctggc acttccccac aaccagcaca ggcttccact tggcccct	400
25	Met	
	tgatcaggat caagcaggca cttcaagcct caataggacc aaggtgctgg ggtgttcccc	460
	tcccaacctg gtgttcaagc atggttctct ggcgccccag gccttgcttc cctggcctgc	520
	tgggggggttc cgggtctcca gaaggacatg gtgctggtcc ctcccttagc ccaagggaga	580
30	ggcaataaag acacaaagct g	601

<210> 29

<211> 585

<212> DNA

35 <213> Homo sapiens

28/177

<220>

<221> CDS

<222> (78)...(452)

5 <400> 29
 actaacctct gccctgcagc cgcgagggcg cgcgggaaat cccgagtgc tctggaatac 60
 gcagagtcag taagacc atg gct acg tcc tcg atg tct aag ggt tgc ttt 110
 Met Ala Thr Ser Ser Met Ser Lys Gly Cys Phe
 1 5 10
 10 gtt ttt aag cca aac tcc aaa aag aga aag atc tct ctg cca ata gag 158
 Val Phe Lys Pro Asn Ser Lys Lys Arg Lys Ile Ser Leu Pro Ile Glu
 15 15 20 25
 gac tat ttt aac aaa ggg aaa aat gag cct gag gac agt aag ctt cga 206
 Asp Tyr Phe Asn Lys Gly Lys Asn Glu Pro Glu Asp Ser Lys Leu Arg
 15 30 35 40
 ttc gaa act tat cag ttg ata tgg cag cag atg aaa tct gaa aat gag 254
 Phe Glu Thr Tyr Gln Leu Ile Trp Gln Gln Met Lys Ser Glu Asn Glu
 45 50 55
 cga cta caa gag gaa tta aat aaa aac ttg ttt gac aat ctg att gaa 302
 20 Arg Leu Gln Glu Glu Leu Asn Lys Asn Leu Phe Asp Asn Leu Ile Glu
 60 65 70 75
 ttt ctg caa aaa tca cat tct gga ttc cag aag aat tca aga gac ttg 350
 Phe Leu Gln Lys Ser His Ser Gly Phe Gln Lys Asn Ser Arg Asp Leu
 80 85 90
 25 ggc ggt caa ata aaa ctc aga gaa att cca act gct gct ctt gtt ctt 398
 Gly Gly Gln Ile Lys Leu Arg Glu Ile Pro Thr Ala Ala Leu Val Leu
 95 100 105
 ggt ata tat gcg tat gtt tgt tca tgc atg cat ctc tgt gta ttt cgt 446
 Gly Ile Tyr Ala Tyr Val Cys Ser Cys Met His Leu Cys Val Phe Arg
 110 115 120
 30 ttt taaatttttt tttattgttg agaatagtgg aaggacctgt tttgatgagc c 500
 Phe
 tattttgtct ctcttatttg tacaattaaa ccaactatag tttatattac atattttcaa 560
 35 aaaccaataa aaattcctta tcttt 585

29/177

<210> 30
 <211> 1100
 <212> DNA
 5 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (57)...(1040)

10 <400> 30
 agaccgacct tgaccgccca cctggcagga gcaggacagg acggccggac gcggcc atg 59
 Met
 1
 gcc gag ctc ccg ggg ccc ttt ctc tgc ggg gcc ctg cta ggc ttc ctg 107
 15 Ala Glu Leu Pro Gly Pro Phe Leu Cys Gly Ala Leu Leu Gly Phe Leu
 5 10 15
 tgc ctg agt ggg ctg gcc gtg gag gtg aag gta ccc aca gag ccg ctg 155
 Cys Leu Ser Gly Leu Ala Val Glu Val Lys Val Pro Thr Glu Pro Leu
 20 25 30
 20 agc acg ccc ctg ggg aag aca gcc gag ctg acc tgc acc tac agc acg 203
 Ser Thr Pro Leu Gly Lys Thr Ala Glu Leu Thr Cys Thr Tyr Ser Thr
 35 40 45
 tcg gtg gga gac agc ttc gcc ctg gag tgg agc ttt gtg cag cct ggg 251
 Ser Val Gly Asp Ser Phe Ala Leu Glu Trp Ser Phe Val Gln Pro Gly
 25 50 55 60 65
 aaa ccc atc tct gag tcc cat cca atc ctg tac ttc acc aat ggc cat 299
 Lys Pro Ile Ser Glu Ser His Pro Ile Leu Tyr Phe Thr Asn Gly His
 70 75 80
 ctg tat cca act ggt tct aag tca aag cgg gtc agc ctg ctt cag aac 347
 30 Leu Tyr Pro Thr Gly Ser Lys Ser Lys Arg Val Ser Leu Leu Gln Asn
 85 90 95
 ccc ccc aca gtg ggg gtg gcc aca ctg aaa ctg act gac gtc cac ccc 395
 Pro Pro Thr Val Gly Val Ala Thr Leu Lys Leu Thr Asp Val His Pro
 100 105 110
 35 tca gat act gga acc tac ctc tgc caa gtc aac aac cca cca gat ttc 443

30/177

	Ser Asp Thr Gly Thr Tyr Leu Cys Gln Val Asn Asn Pro Pro Asp Phe			
	115	120	125	
	tac acc aat ggg ttg ggg cta atc aac ctt act gtg ctg gtt ccc ccc		491	
	Tyr Thr Asn Gly Leu Gly Leu Ile Asn Leu Thr Val Leu Val Pro Pro			
5	130	135	140	145
	agt aat ccc tta tgc agt cag agt gga caa acc tct gtg gga ggc tct			539
	Ser Asn Pro Leu Cys Ser Gln Ser Gly Gln Thr Ser Val Gly Gly Ser			
	150	155	160	
	act gca ctg aga tgc agc tct tcc gag ggg gct cct aag cca gtg tac			587
10	Thr Ala Leu Arg Cys Ser Ser Ser Glu Gly Ala Pro Lys Pro Val Tyr			
	165	170	175	
	aac tgg gtg cgt ctt gga act ttt cct aca cct tct cct ggc agc atg			635
	Asn Trp Val Arg Leu Gly Thr Phe Pro Thr Pro Ser Pro Gly Ser Met			
	180	185	190	
15	gtt caa gat gag gtg tct ggc cag ctc att ctc acc aac ctc tcc ctg			683
	Val Gln Asp Glu Val Ser Gly Gln Leu Ile Leu Thr Asn Leu Ser Leu			
	195	200	205	
	acc tcc tcg ggc acc tac cgc tgt gtg gcc acc aac cag atg ggc agt			731
	Thr Ser Ser Gly Thr Tyr Arg Cys Val Ala Thr Asn Gln Met Gly Ser			
20	210	215	220	225
	gca tcc tgt gag ctg acc ctc tct gtg acc gaa ccc tcc caa ggc cga			779
	Ala Ser Cys Glu Leu Thr Leu Ser Val Thr Glu Pro Ser Gln Gly Arg			
	230	235	240	
	gtg gcc gga gct ctg att ggg gtg ctc ctg ggc gtg ctg ttg ctg tca			827
25	Val Ala Gly Ala Leu Ile Gly Val Leu Leu Gly Val Leu Leu Leu Ser			
	245	250	255	
	gtt gct gcg ttc tgc ctg gtc agg ttc cag aaa gag agg ggg aag aag			875
	Val Ala Ala Phe Cys Leu Val Arg Phe Gln Lys Glu Arg Gly Lys Lys			
	260	265	270	
30	ccc aag gag aca tat ggg ggt agt gac ctt cgg gag gat gcc atc gct			923
	Pro Lys Glu Thr Tyr Gly Gly Ser Asp Leu Arg Glu Asp Ala Ile Ala			
	275	280	285	
	cct ggg atc tct gag cac act tgt atg agg gct gat tct agc aag ggg			971
	Pro Gly Ile Ser Glu His Thr Cys Met Arg Ala Asp Ser Ser Lys Gly			
35	290	295	300	305

31/177

ttc ctg gaa aga ccc tcg tct gcc agc acc gtg acg acc acc aag tcc 1019

Phe Leu Glu Arg Pro Ser Ser Ala Ser Thr Val Thr Thr Thr Lys Ser

310

315

320

aag ctc cct atg gtc gtg tgacttctcc cgatccctga gggcggtgag ggg 1070

5 Lys Leu Pro Met Val Val

325

gaatatcaat aattaaagtc tgtgggtacc 1100

<210> 31

10 <211> 313

<212> PRT

<213> Homo sapiens

<400> 31

15 Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg Gly

1

5

10

15

Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr Cys Ser

20

25

30

Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys Asp Glu Cys

20 35

40

45

Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr Glu Asn Gly Val

50

55

60

Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly Gly Gly Gly Trp Thr

65

70

75

80

25 Leu Val Ala Ser Val His Glu Asn Asp Met Arg Gly Lys Cys Thr Val

85

90

95

Gly Asp Arg Trp Ser Ser Gln Gln Gly Ser Lys Ala Asp Tyr Pro Glu

100

105

110

Gly Asp Gly Asn Trp Ala Asn Tyr Asn Thr Phe Gly Ser Ala Glu Ala

30 115

120

125

Ala Thr Ser Asp Asp Tyr Lys Asn Pro Gly Tyr Tyr Asp Ile Gln Ala

130

135

140

Lys Asp Leu Gly Ile Trp His Val Pro Asn Lys Ser Pro Met Gln His

145

150

155

160

35 Trp Arg Asn Ser Ser Leu Leu Arg Tyr Arg Thr Asp Thr Gly Phe Leu

32/177

165 170 175
 Gln Thr Leu Gly His Asn Leu Phe Gly Ile Tyr Gln Lys Tyr Pro Val
 180 185 190
 Lys Tyr Gly Glu Gly Lys Cys Trp Thr Asp Asn Gly Pro Val Ile Pro
 5 195 200 205
 Val Val Tyr Asp Phe Gly Asp Ala Gln Lys Thr Ala Ser Tyr Tyr Ser
 210 215 220
 Pro Tyr Gly Gln Arg Glu Phe Thr Ala Gly Phe Val Gln Phe Arg Val
 225 230 235 240
 10 Phe Asn Asn Glu Arg Ala Ala Asn Ala Leu Cys Ala Gly Met Arg Val
 245 250 255
 Thr Gly Cys Asn Thr Glu His His Cys Ile Gly Gly Gly Tyr Phe
 260 265 270
 Pro Glu Ala Ser Pro Gln Gln Cys Gly Asp Phe Ser Gly Phe Asp Trp
 15 275 280 285
 Ser Gly Tyr Gly Thr His Val Gly Tyr Ser Ser Ser Arg Glu Ile Thr
 290 295 300
 Glu Ala Ala Val Leu Leu Phe Tyr Arg
 305 310
 20
 <210> 32
 <211> 229
 <212> PRT
 <213> Homo sapiens
 25
 <400> 32
 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
 1 5 10 15
 Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
 30 20 25 30
 Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
 35 40 45
 Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
 50 55 60
 35 Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu

33/177

65 70 75 80
 Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
 85 90 95
 Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
 5 100 105 110
 Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
 115 120 125
 Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
 130 135 140
 10 Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile
 145 150 155 160
 Asn Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu
 165 170 175
 Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe
 15 180 185 190
 Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
 195 200 205
 Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys
 210 215 220
 20 Arg Lys Ser Arg Thr
 225

 <210> 33
 <211> 467
 25 <212> PRT
 <213> Homo sapiens

 <400> 33
 Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
 30 1 5 10 15
 Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
 20 25 30
 Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
 35 40 45
 35 Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe

34/177

	50	55	60
	Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys		
	65	70	75 80
5	Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro	85	90 95
	Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe	100	105 110
	Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr	115	120 125
10	Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser	130	135 140
	Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp	145	150 155 160
	Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg	165	170 175
15	Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu	180	185 190
	Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys	195	200 205
20	Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val	210	215 220
	Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser	225	230 235 240
	Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr	245	250 255
25	Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly	260	265 270
	Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro	275	280 285
30	His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr	290	295 300
	Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val	305	310 315 320
	Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn	325	330 335
35			

35/177

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
 340 345 350
 Leu Arg Gln Met Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
 355 360 365
 5 Glu Thr His Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380
 Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
 385 390 395 400
 Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
 10 405 410 415
 Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
 420 425 430
 Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
 435 440 445
 15 Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
 450 455 460
 Asn Val Ile
 465

 20 <210> 34
 <211> 99
 <212> PRT
 <213> Homo sapiens

 25 <400> 34
 Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
 1 5 10 15
 Val Lys Gly His Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu
 20 25 30
 30 Val Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro
 35 40 45
 Glu Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr
 50 55 60
 Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
 35 65 70 75 80

36/177

Phe Asn Pro Ser Gly Pro Tyr Gln Gln Lys Pro Val His Glu Lys Lys
 85 90 95

Glu Val Leu

5 <210> 35
 <211> 189
 <212> PRT
 <213> Homo sapiens

10 <400> 35
 Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
 1 5 10 15
 Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
 20 25 30
 15 Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu
 35 40 45
 Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys
 50 55 60
 Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln
 20 65 70 75 80
 Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu
 85 90 95
 Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala
 100 105 110
 25 Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly
 115 120 125
 Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg
 130 135 140
 Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr
 30 145 150 155 160
 His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly
 165 170 175
 Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser Leu
 180 185

35

37/177

<210> 36

<211> 363

<212> PRT

<213> Homo sapiens

5

<400> 36

Met Val Asp Ser Leu Leu Ala Val Thr Leu Ala Gly Asn Leu Gly Leu
 1 5 10 15
 Thr Phe Leu Arg Gly Ser Gln Thr Gln Ser His Pro Asp Leu Gly Thr
 10 20 25 30
 Glu Gly Cys Trp Asp Gln Leu Ser Ala Pro Arg Thr Phe Thr Leu Leu
 35 40 45
 Asp Pro Lys Ala Ser Leu Leu Thr Lys Ala Phe Leu Asn Gly Ala Leu
 50 55 60
 15 Asp Gly Val Ile Leu Gly Asp Tyr Leu Ser Arg Thr Pro Glu Pro Arg
 65 70 75 80
 Pro Ser Leu Ser His Leu Leu Ser Gln Tyr Tyr Gly Ala Gly Val Ala
 85 90 95
 Arg Asp Pro Gly Phe Arg Ser Asn Phe Arg Arg Gln Asn Gly Ala Ala
 100 105 110
 20 Leu Thr Ser Ala Ser Ile Leu Ala Gln Gln Val Trp Gly Thr Leu Val
 115 120 125
 Leu Leu Gln Arg Leu Glu Pro Val His Leu Gln Leu Gln Cys Met Ser
 130 135 140
 25 Gln Glu Gln Leu Ala Gln Val Ala Ala Asn Ala Thr Lys Glu Phe Thr
 145 150 155 160
 Glu Ala Phe Leu Gly Cys Pro Ala Ile His Pro Arg Cys Arg Trp Gly
 165 170 175
 Ala Ala Pro Tyr Arg Gly Arg Pro Lys Leu Leu Gln Leu Pro Leu Gly
 180 185 190
 30 Phe Leu Tyr Val His His Thr Tyr Val Pro Ala Pro Pro Cys Thr Asp
 195 200 205
 Phe Thr Arg Cys Ala Ala Asn Met Arg Ser Met Gln Arg Tyr His Gln
 210 215 220
 35 Asp Thr Gln Gly Trp Gly Asp Ile Gly Tyr Ser Phe Val Val Gly Ser

38/177

225 230 235 240
 Asp Gly Tyr Val Tyr Glu Gly Arg Gly Trp His Trp Val Gly Ala His
 245 250 255
 Thr Leu Gly His Asn Ser Arg Gly Phe Gly Val Ala Ile Val Gly Asn
 5 260 265 270
 Tyr Thr Ala Ala Leu Pro Thr Glu Ala Ala Leu Arg Thr Val Arg Asp
 275 280 285
 Thr Leu Pro Ser Cys Ala Val Arg Ala Gly Leu Leu Arg Pro Asp Tyr
 290 295 300
 10 Ala Leu Leu Gly His Arg Gln Leu Val Arg Thr Asp Cys Pro Gly Asp
 305 310 315 320
 Ala Leu Phe Asp Leu Leu Arg Thr Trp Pro His Phe Thr Ala Thr Val
 325 330 335
 Lys Pro Arg Pro Ala Arg Ser Val Ser Lys Arg Ser Arg Arg Glu Pro
 15 340 345 350
 Pro Pro Arg Thr Leu Pro Ala Thr Asp Leu Gln
 355 360

 <210> 37
 20 <211> 249
 <212> PRT
 <213> Homo sapiens

 <400> 37
 25 Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu
 1 5 10 15
 Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
 20 25 30
 Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp
 30 35 40 45
 Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln
 50 55 60
 Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu
 65 70 75 80
 35 Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln

39/177

	85	90	95
	Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile		
	100	105	110
5	Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn		
	115	120	125
	Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Val Gln Val		
	130	135	140
	Leu Lys Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly		
	145	150	155
10	Leu Leu Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser		
	165	170	175
	His Val Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn		
	180	185	190
	Ile Lys Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr		
15	195	200	205
	Phe Thr Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala		
	210	215	220
	Gln Lys Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu		
	225	230	235
20	Lys Val Val Thr Ile Ile Pro Lys Ile		
	245		
	<210> 38		
	<211> 98		
25	<212> PRT		
	<213> Homo sapiens		
	<400> 38		
	Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile		
30	1	5	10
	Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe		
	20	25	30
	Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu		
	35	40	45
35	Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu Gln		

```

50          55          60
Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly
  65          70          75          80
Gly Phe Ser Phe Cys Gln Val Arg Leu Asn Lys Arg Lys Glu Tyr Met
5          85          90          95
Val Arg

<210> 39
<211> 172
10 <212> PRT
    <213> Homo sapiens

<400> 39
Met Val Gly Pro Ala Pro Arg Arg Arg Leu Arg Pro Leu Ala Ala Leu
15      1          5          10          15
Ala Leu Val Leu Ala Leu Ala Pro Gly Leu Pro Thr Ala Arg Ala Gly
      20          25          30
Gln Thr Pro Arg Pro Ala Glu Arg Gly Pro Pro Val Arg Leu Phe Thr
      35          40          45
20 Glu Glu Glu Leu Ala Arg Tyr Gly Gly Glu Glu Glu Asp Gln Pro Ile
      50          55          60
Tyr Leu Ala Val Lys Gly Val Val Phe Asp Val Thr Ser Gly Lys Glu
      65          70          75          80
Phe Tyr Gly Arg Gly Ala Pro Tyr Asn Ala Leu Thr Gly Lys Asp Ser
25          85          90          95
Thr Arg Gly Val Ala Lys Met Ser Leu Asp Pro Ala Asp Leu Thr His
      100          105          110
Asp Thr Thr Gly Leu Thr Ala Lys Glu Leu Glu Ala Leu Asp Glu Val
      115          120          125
30 Phe Thr Lys Val Tyr Lys Ala Lys Tyr Pro Ile Val Gly Tyr Thr Ala
      130          135          140
Arg Arg Ile Leu Asn Glu Asp Gly Ser Pro Asn Leu Asp Phe Lys Pro
      145          150          155          160
Glu Asp Gln Pro His Phe Asp Ile Lys Asp Glu Phe
35          165          170

```

41/177

<210> 40

<211> 120

<212> PRT

5 <213> Homo sapiens

<400> 40

Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys
 1 5 10 15
 10 Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu
 20 25 30
 Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu
 35 40 45
 Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser
 15 50 55 60
 Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val
 65 70 75 80
 Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His
 85 90 95
 20 Leu Arg Ile Ala Tyr Tyr Ala Ser Lys Gly Tyr Arg Gly Tyr Ser Tyr
 100 105 110
 Asp Asp Ile Pro Asp Phe Asp Asp
 115 120

25 <210> 41

<211> 939

<212> DNA

<213> Homo sapiens

30 <400> 41

atgaaccaac tcagcttcct gctgtttctc atagcgacca ccagaggatg gagtacagat 60
 gaggctaata cttacttcaa ggaatggacc tgttcttcgt ctccatctct gccagaagc 120
 tgcaaggaaa tcaaagacga atgtcctagt gcatttgatg gcctgtatct tctccgcact 180
 gagaatggtg ttatctacca gaccttctgt gacatgacct ctgggggtgg cggctggacc 240
 35 ctggtggcca gcgatcatga gaatgacatg cgtgggaagt gcacgggtgg cgatcgctgg 300

42/177

tccagtcagc agggcagcaa agcagactac ccagaggggg acggcaactg ggccaactac 360
 aacacctttg gatctgcaga ggcggccacg agcgatgact acaagaaccc tggtactac 420
 gacatccagg ccaaggacct gggcatctgg cactgcccc ataagtcccc catgcagcac 480
 tggagaaaca gctccctgct gaggtaccgc acggacactg gcttctcca gacactggga 540
 5 cataatctgt ttggcatcta ccagaaatat ccagtgaat atggagaagg aaagtgttg 600
 actgacaacg gcccggtgat ccctgtggtc tatgattttg gcgacgcca gaaaacagca 660
 tcttattact caccctatgg ccagcgggaa ttcactgagg gatttgttca gttagggta 720
 ttaataacg agagagcagc caacgccttg tgtgctggaa tgagggtcac cggatgtaac 780
 actgagcacc actgcattgg tggaggagga tactttccag aggcagtc ccagcagtgt 840
 10 ggagattttt ctggttttga ttggagtggg tatggaactc atgttggtta cagcagcagc 900
 cgtgagataa ctgaggcagc tgtgcttcta ttctatcgt 939

<210> 42

<211> 687

15 <212> DNA

<213> Homo sapiens

<400> 42

atgggcgaca agatctggct gcccttcccc gtgtccttc tggccgctct gcctccggtg 60
 20 ctgctgectg gggcgcccg cttcacacct tccctcgata gcgaactcac ctttaccctt 120
 cccgccggcc agaaggagt cttctaccag cccatgcccc tgaaggcctc gctggagatc 180
 gagtaccag ttttagatgg agcaggatta gatattgatt tccatcttgc ctctccagaa 240
 ggcaaaacct tagtttttga acaagaaaa tcagatggag ttcacactgt agagactgaa 300
 gttggtgatt acatgttctg ctttgacaat acattcagca ccatttctga gaagggtgatt 360
 25 ttctttgaat taatcctgga taatatggga gaacaggcac aagaacaaga agattggaag 420
 aaatatatta ctggcacaga tatattggat atgaaactgg aagacatcct ggaatccatc 480
 aacagcatca agtccagact aagcaaaagt gggcacatac aaattctgct tagagcattt 540
 gaagctcgtg atcgaaacat acaagaaagc aactttgata gagtcaattt ctggtctatg 600
 gttaatttag tggteatggg ggtggtgtca gccattcaag tttatatgct gaagagtctg 660
 30 tttgaagata agaggaaaag tagaact 687

<210> 43

<211> 1401

<212> DNA

35 <213> Homo sapiens

43/177

	<400> 43	
	atgcgggcccc agggagctccc caggctcgcg ttcccgttgc tgetgttget gttgetgetg	60
	ctgccgcccgc cgcctgtccc tgcccacagc gccacgeget tcgaccccac ctgggagtc	120
5	ctggacgccc gccagctgce cgcgtggttt gaccaggcca agttcggeat cttcatccac	180
	tggggagtgt tttccgtgcc cagcttcggt agcgagtggg tctggtggta ttggcaaaag	240
	gaaaagatac cgaagtatgt ggaatttatg aaagataatt accctcctag tttcaaatat	300
	gaagattttg gaccactatt tacagcaaaa ttttttaatg ccaaccagtg ggcagatatt	360
	tttcaggcct ctggtgccaa atacattgtc ttaacttcca aacatcatga aggctttacc	420
10	ttgtgggggt cagaatattc gtggaactgg aatgccatag atgagggggc caagagggac	480
	attgtcaagg aacttgagg agccattagg aacagaactg acctgcgttt tggactgtac	540
	tattcccttt ttgaatggtt tcatccgctc ttccctgagg atgaatccag ttcattccat	600
	aagcggcaat ttccagtttc taagacattg ccagagctct atgagttagt gaacaactat	660
	cagcctgagg ttctgtggtc ggatggtgac ggaggagcac cggatcaata ctggaacagc	720
15	acaggcttct tggcctgggt atataatgaa agcccagttc ggggcacagt agtcaccaat	780
	gatcgttggg gagctggtag catctgtaag catggtggct tctatacctg cagtgategt	840
	tataaccag gacatctttt gccacataaa tgggaaaact gcatgacaat agacaaactg	900
	tcctggggct ataggaggga agctggaatc tctgactatc ttacaattga agaattggtg	960
	aagcaacttg tagagacagt ttcatgtgga ggaaatcttt tgatgaatat tgggcccaca	1020
20	ctagatggca ccattttctgt agtttttgag gagcgactga ggcaaattgg gtccctggcta	1080
	aaagtcaatg gagaagctat ttatgaaacc catacctggc gatcccagaa tgacactgtc	1140
	acccagatg tgtggtacac atccaagcct aaagaaaaat tagtctatgc catttttctt	1200
	aatggccca catcaggaca gctgttctt ggccatccca aagctattct gggggcaaca	1260
	gaggtgaaac tactgggcca tggacagcca cttaactgga tttctttgga gcaaaatggc	1320
25	attatggtag aactgccaca gctaaccatt catcagatgc cgtgtaaatg gggctgggct	1380
	ctagccctga ctaatgtgat c	1401
	<210> 44	
	<211> 297	
30	<212> DNA	
	<213> Homo sapiens	
	<400> 44	
	atggataacg tgcagccgaa aataaaacat cgccccttct gcttcagtgt gaaaggccac	60
35	gtgaagatgc tgcggctgga tattatcaac tcaactggtaa caacagtatt catgtcctc	120

44/177

gtatctgtgt tggcactgat accagaaacc acaacattga cagttggtgg aggggtgttt 180
gcacttgtga cagcagtatg ctgtottgcc gacggggccc ttatttaccg gaagcttctg 240
ttcaatccca gcggctctta ccagcaaaag cctgtgcatg aaaaaaaga agttttg 297

5 <210> 45
<211> 567
<212> DNA
<213> Homo sapiens

10 <400> 45
atggaggaag gcgggaacct aggaggcctg attaagatgg tccatctact ggtcttgtca 60
ggtgcctggg gcatgcaa atgtgggtgacc ttctgtctcag gcttcctget tttccgaagc 120
cttccccgac ataccttcgg actagtgcag agcaaactct tccccctcta cttccacatc 180
tccatggggt gtgccttcat caacctctgc atcttggtt cacagcatgc ttgggctcag 240
15 ctcacattct gggaggccag ccagctttac ctgctgttcc tgagccttac gctggccact 300
gtcaacgccc gctggctgga accccgcacc acagctgcca tgtgggcccct gcaaaccgtg 360
gagaaggagc gaggcctggg tggggaggtta ccaggcagcc accagggtcc cgatccctac 420
cgccagctgc gagagaagga cccaagtac agtgcctctc gccagaattt cttccgctac 480
catgggctgt cctctctttg caatctgggc tgcgtcctga gcaatgggct ctgtctcgt 540
20 ggccttgccc tggaaataag gacccctc 567

<210> 46

<211> 1089

<212> DNA

25 <213> Homo sapiens

<400> 46
atggtggaca gcctcctggc agtcaccctg gctggaaacc tgggcctgac cttcctccga 60
ggttcccaga ccagagcca tccagacctg ggaactgagg gctgctggga ccagctctct 120
30 gccctcgga cctttacgt tttggacccc aaggcatctc tgttaaccaa ggcccttctc 180
aatggcgccc tggatggggt catccttgga gactacctga gccggactcc tgagccccgg 240
ccatccctca gccacttgct gagccagtac tatggggctg ggggtggccag agaccaggg 300
ttccgcagca acttccgacg gcagaacggt gctgctctga cttcagcctc catcctggcc 360
cagcaggtgt ggggaacctt tgctcttcta cagaggctgg agccagtaca cctccagctt 420
35 cagtgcctga gccaaagaaca gctggcccag gtggctgcca atgetaccaa ggaattcact 480

45/177

	gaggcettcc tgggatgecc ggccatccac ccccgtgcc gctggggagc ggcgccttat	540
	eggggcccgc cgaagetgct gcagetgccg ctgggattct tgtacgtgca tcacacctac	600
	gtgcctgcac caccctgcac ggacttcacg cgtgcgcag ccaacatgcg ctccatgcag	660
	cgtaccacc aggacacgca aggetgggga gacatcgget acagtttcgt ggtgggctcg	720
5	gacggctacg tgtacgaggg acgcggctgg cactgggtgg gcgcccacac gctcgggcac	780
	aactcccggg gcttcggcgt ggccatagtg ggcaactaca ccgcggcgt gccacccgag	840
	gccgctctgc gcacggtgcg cgacacgctc ccgagttgtg cgggtgcgcg cggcctcctg	900
	cggccagact acgcgtgct gggccaccgc cagctggtgc gcaccgactg ccccggcgac	960
	gcgtcttcg acctgctgcg cacttgccg cacttcaccg cgactgttaa gccaaagact	1020
10	gccaggagtg tctctaagag atccaggagg gagccacccc caaggaccct gccagccaca	1080
	gacctccaa	1089
	<210> 47	
	<211> 747	
15	<212> DNA	
	<213> Homo sapiens	
	<400> 47	
	atgggtggcc cccggggcgc gggetgggtg gcggcgggce tgctgctcgg cgcgggcgcc	60
20	tgctactgca ttacagget gaccgggggt cggcggcggg gcgaccgcga gctcgggata	120
	cgtcttcoga agtcgcgaga agacttaact gatggttcat atgatgatgt tctaaatgct	180
	gaacaacttc agaaactcct ttacctgctg gagtcaacgg aggatcctgt aattattgaa	240
	agagctttga ttactttggg taacaatgca gccttttcag ttaaccaagc tattattcgt	300
	gaattgggtg gtattccaat tgttgcaaac aaaatcaacc attccaacca gagtattaaa	360
25	gagaaagctt taaatgcact aaataacctg agtgtgaatg ttgaaaatca aatcaagata	420
	aagggtgcaag ttttgaaact gcttttgaaat ttgtctgaaa atccagccat gacagaagga	480
	cttctccgtg cccaagtgga ttcattcatt ctttcccttt atgacagcca cgtagcaaaag	540
	gagattcttc ttcgagtact tacgtattt cagaatataa agaactgcct caaaatagaa	600
	ggccatttag ctgtgcagcc tactttcact gaaggttcat tgtttttctt gttacatgga	660
30	gaagaatgtg ccagaaaaat aagagcttta gttgatcacc atgatgcaga ggtgaaggaa	720
	aaggttgtaa caataatacc caaaatc	747
	<210> 48	
	<211> 294	
35	<212> DNA	

46/177

<213> Homo sapiens

<400> 48

5 atggcgctgc tctgtgctg tgggcgaag ctggccgct gggcatcgt cctcagcgcc 60
 tggggagtga tcatgttgat aatgctcgga atatttttca atgtccattc cgctgtgttg 120
 attgaggacg ttcccttcac ggagaaagat tttgagaatg gccccagaa catatacaac 180
 ctttacgagc aagtcagcta caactgtttc atcgtgcag gcctttacct cctcctcgga 240
 ggcttctctt tctgccaagt tcggctcaat aagcgcaagg aatacatggt gcgc 294

10 <210> 49

<211> 516

<212> DNA

<213> Homo sapiens

15 <400> 49

atggtgggcc ccgcgccgcg gcggcggtg cgcccgctgg cagcgctggc cctggtcctg 60
 gcgctggccc cggggctgcc cacagcccgg gccgggcaga caccgcgcc tgccgagcgg 120
 gggccccag tgcggctttt caccgaggag gagctggccc gctatggcgg ggaggaggaa 180
 gatcagccca totacttggc agtgaaggga gtggtgtttg atgtcacctc cggaaaggag 240
 20 ttttatggac gaggagcccc ctacaatgcc ttgacgggga aggactccac tagaggggta 300
 gccaatgt ccttggatec tgcagacctc acccatgaca ctacgggtct cagggccaag 360
 gaactggagg ccttgatga ggtcttcacc aaagtgtaca aagccaaata ccccatcgtc 420
 ggctacactg ccgggagaat totcaatgag gatggcagcc ctaacctgga cttcaagcct 480
 gaagaccagc ccatttttga catcaaggat gagtte 516

25

<210> 50

<211> 360

<212> DNA

<213> Homo sapiens

30

<400> 50

atgatgccgt ccgtaccaa cctggetact ggaatcccca gtagtaaagt gaaatattca 60
 aggetctcca gcacagacga tggctacatt gaccttcagt ttaagaaaac cctcctaag 120
 atcccttata aggccatcgc acttgccact gtgctgtttt tgattggcgc ctttctcatt 180
 35 attataggct cctcctgct gtcaggctac atcagcaaag ggggggcaga ccgggccgtt 240

47/177

ccagtgetga tcattggcat tctggtgttc ctaccggat tttaccacct ggcateget 300
tactatgcat ccaaaggcta ccgtggttac tcctatgatg acattccaga ctttgatgac 360

<210> 51

5 <211> 1065

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

10 <222> (2)...(943)

<400> 51

a atg aac caa ctc agc ttc ctg ctg ttt ctc ata gcg acc acc aga gga 49
Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg Gly

15 1 5 10 15
tgg agt aca gat gag gct aat act tac ttc aag gaa tgg acc tgt tct 97
Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr Cys Ser

20 20 25 30
tcg tct cca tct ctg ccc aga agc tgc aag gaa atc aaa gac gaa tgt 145
Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys Asp Glu Cys

25 35 40 45
cct agt gca ttt gat ggc ctg tat ttt ctc cgc act gag aat ggt gtt 193
Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr Glu Asn Gly Val

50 55 60
atc tac cag acc ttc tgt gac atg acc tct ggg ggt ggc ggc tgg acc 241
Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly Gly Gly Gly Trp Thr

65 70 75 80
ctg gtg gcc agc gtg cat gag aat gac atg cgt ggg aag tgc acg gtg 289
Leu Val Ala Ser Val His Glu Asn Asp Met Arg Gly Lys Cys Thr Val

30 85 90 95
ggc gat cgc tgg tcc agt cag cag ggc agc aaa gca gac tac cca gag 337
Gly Asp Arg Trp Ser Ser Gln Gln Gly Ser Lys Ala Asp Tyr Pro Glu

100 105 110
ggg gac ggc aac tgg gcc aac tac aac acc ttt gga tct gca gag gcg 385
Gly Asp Gly Asn Trp Ala Asn Tyr Asn Thr Phe Gly Ser Ala Glu Ala

48/177

	115	120	125	
	gcc acg agc gat gac tac aag aac cct ggc tac tac gac atc cag gcc			433
	Ala Thr Ser Asp Asp Tyr Lys Asn Pro Gly Tyr Tyr Asp Ile Gln Ala			
	130	135	140	
5	aag gac ctg ggc atc tgg cac gtg ccc aat aag tcc ccc atg cag cac			481
	Lys Asp Leu Gly Ile Trp His Val Pro Asn Lys Ser Pro Met Gln His			
	145	150	155	160
	tgg aga aac agc tcc ctg ctg agg tac cgc acg gac act ggc ttc ctc			529
	Trp Arg Asn Ser Ser Leu Leu Arg Tyr Arg Thr Asp Thr Gly Phe Leu			
10	165	170	175	
	cag aca ctg gga cat aat ctg ttt ggc atc tac cag aaa tat cca gtg			577
	Gln Thr Leu Gly His Asn Leu Phe Gly Ile Tyr Gln Lys Tyr Pro Val			
	180	185	190	
	aaa tat gga gaa gga aag tgt tgg act gac aac ggc ccg gtg atc cct			625
15	Lys Tyr Gly Glu Gly Lys Cys Trp Thr Asp Asn Gly Pro Val Ile Pro			
	195	200	205	
	gtg gtc tat gat ttt ggc gac gcc cag aaa aca gca tct tat tac tca			673
	Val Val Tyr Asp Phe Gly Asp Ala Gln Lys Thr Ala Ser Tyr Tyr Ser			
	210	215	220	
20	ccc tat ggc cag cgg gaa ttc act gcg gga ttt gtt cag ttc agg gta			721
	Pro Tyr Gly Gln Arg Glu Phe Thr Ala Gly Phe Val Gln Phe Arg Val			
	225	230	235	240
	ttt aat aac gag aga gca gcc aac gcc ttg tgt gct gga atg agg gtc			769
	Phe Asn Asn Glu Arg Ala Ala Asn Ala Leu Cys Ala Gly Met Arg Val			
25	245	250	255	
	acc gga tgt aac act gag cac cac tgc att ggt gga gga gga tac ttt			817
	Thr Gly Cys Asn Thr Glu His His Cys Ile Gly Gly Gly Tyr Phe			
	260	265	270	
	cca gag gcc agt ccc cag cag tgt gga gat ttt tct ggt ttt gat tgg			865
30	Pro Glu Ala Ser Pro Gln Gln Cys Gly Asp Phe Ser Gly Phe Asp Trp			
	275	280	285	
	agt gga tat gga act cat gtt ggt tac agc agc agc cgt gag ata act			913
	Ser Gly Tyr Gly Thr His Val Gly Tyr Ser Ser Ser Arg Glu Ile Thr			
	290	295	300	
35	gag gca gct gtg ctt cta ttc tat cgt tgagagtttt gtgggagggga			960

49/177

Glu Ala Ala Val Leu Leu Phe Tyr Arg

305

310

accagacct ctctcccaa ccatgagatc ccaaggatgg agaacaactt acccagtagc 1020

tagaatgtta atggcagaag agaaaacaat aaatcatatt gactc 1065

5

<210> 52

<211> 937

<212> DNA

<213> Homo sapiens

10

<220>

<221> CDS

<222> (177)...(866)

<400> 52

15 cttttggaga actgegettc tctttcggag ggagtgttcg ccgcccgcgc ggcccgcacc 60

tggagtttct tcagactcca gatttccttg tcaaccacga ggagtccaga gaggaaacgc 120

ggagcggaga caacagtacc tgacgcctct ttcagcccgg gatcgcccca gcaggg 176

atg ggc gac aag atc tgg ctg ccc ttc ccc gtg ctc ctt ctg gcc get 224

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala

20

1

5

10

15

ctg cct ccg gtg ctg ctg cct ggg gcg gcc ggc ttc aca cct tcc ctc 272

Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu

20

25

30

gat agc gac ttc acc ttt acc ctt ccc gcc ggc cag aag gag tgc ttc 320

25

Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe

35

40

45

tac cag ccc atg ccc ctg aag gcc tcg ctg gag atc gag tac caa gtt 368

Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val

50

55

60

30

tta gat gga gca gga tta gat att gat ttc cat ctt gcc tct cca gaa 416

Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu

65

70

75

80

ggc aaa acc tta gtt ttt gaa caa aga aaa tca gat gga gtt cac act 464

Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr

35

85

90

95

50/177

	gta gag act gaa gtt ggt gat tac atg ttc tgc ttt gac aat aca ttc	512
	Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe	
	100 105 110	
	agc acc att tct gag aag gtg att ttc ttt gaa tta atc ctg gat aat	560
5	Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn	
	115 120 125	
	atg gga gaa cag gca caa gaa caa gaa gat tgg aag aaa tat att act	608
	Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr	
	130 135 140	
10	ggc aca gat ata ttg gat atg aaa ctg gaa gac atc ctg gaa tcc atc	656
	Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile	
	145 150 155 160	
	aac agc atc aag tcc aga cta agc aaa agt ggg cac ata caa att ctg	704
	Asn Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu	
15	165 170 175	
	ctt aga gca ttt gaa got cgt gat cga aac ata caa gaa agc aac ttt	752
	Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe	
	180 185 190	
	gat aga gtc aat ttc tgg tct atg gtt aat tta gtg gtc atg gtg gtg	800
20	Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val	
	195 200 205	
	gtg tca gcc att caa gtt tat atg ctg aag agt ctg ttt gaa gat aag	848
	Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys	
	210 215 220	
25	agg aaa agt aga act taaaactcca aactagagta cgtaacattg aaaaatg	900
	Arg Lys Ser Arg Thr	
	225	
	aggcataaaaa atgcaataaaa ctgttacagt caagacc	937
30	<210> 53	
	<211> 1678	
	<212> DNA	
	<213> Homo sapiens	
	<220>	
35	<221> CDS	

51/177

<222> (56)...(1459)

<400> 53

	agcgcctcccg aggccgcggg agcctgcaga gaggacagcc ggccctgcgcc gggac	55
5	atg cgg ccc cag gag ctc ccc agg ctc gcg ttc ccg ttg ctg ctg ttg	103
	Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu	
	1 5 10 15	
	ctg ttg ctg ctg ctg ccg ccg ccg ccg tgc cct gcc cac agc gcc acg	151
	Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr	
10	20 25 30	
	cgc ttc gac ccc acc tgg gag tcc ctg gac gcc cgc cag ctg ccc gcg	199
	Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala	
	35 40 45	
	tgg ttt gac cag gcc aag ttc ggc atc ttc atc cac tgg gga gtg ttt	247
15	Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe	
	50 55 60	
	tcc gtg ccc agc ttc ggt agc gag tgg ttc tgg tgg tat tgg caa aag	295
	Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys	
	65 70 75 80	
20	gaa aag ata ccg aag tat gtg gaa ttt atg aaa gat aat tac cct cct	343
	Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro	
	85 90 95	
	agt ttc aaa tat gaa gat ttt gga cca cta ttt aca gca aaa ttt ttt	391
	Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe	
25	100 105 110	
	aat gcc aac cag tgg gca gat att ttt cag gcc tct ggt gcc aaa tac	439
	Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr	
	115 120 125	
	att gtc tta act tcc aaa cat cat gaa ggc ttt acc ttg tgg ggg tca	487
30	Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser	
	130 135 140	
	gaa tat tcg tgg aac tgg aat gcc ata gat gag ggg ccc aag agg gac	535
	Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp	
	145 150 155 160	
35	att gtc aag gaa ctt gag gta gcc att agg aac aga act gac ctg cgt	583

52/177

	Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg	
	165 170 175	
	ttt gga ctg tac tat tcc ctt ttt gaa tgg ttt cat ccg ctc ttc ctt	631
	Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu	
5	180 185 190	
	gag gat gaa tcc agt tca ttc cat aag cgg caa ttt cca gtt tct aag	679
	Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys	
	195 200 205	
	aca ttg cca gag ctc tat gag tta gtg aac aac tat cag cct gag gtt	727
10	Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val	
	210 215 220	
	ctg tgg tcg gat ggt gac gga gga gca ccg gat caa tac tgg aac agc	775
	Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser	
	225 230 235 240	
15	aca ggc ttc ttg gcc tgg tta tat aat gaa agc cca gtt cgg ggc aca	823
	Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr	
	245 250 255	
	gta gtc acc aat gat cgt tgg gga gct ggt agc atc tgt aag cat ggt	871
	Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly	
20	260 265 270	
	ggc ttc tat acc tgc agt gat cgt tat aac cca gga cat ctt ttg cca	919
	Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro	
	275 280 285	
	cat aaa tgg gaa aac tgc atg aca ata gac aaa ctg tcc tgg ggc tat	967
25	His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr	
	290 295 300	
	agg agg gaa gct gga atc tct gac tat ctt aca att gaa gaa ttg gtg	1015
	Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val	
	305 310 315 320	
30	aag caa ctt gta gag aca gtt tca tgt gga gga aat ctt ttg atg aat	1063
	Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn	
	325 330 335	
	att ggg ccc aca cta gat ggc acc att tct gta gtt ttt gag gag cga	1111
	Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg	
35	340 345 350	

53/177

	ctg agg caa atg ggg tcc tgg cta aaa gtc aat gga gaa gct att tat	1159
	Leu Arg Gln Met Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr	
	355 360 365	
	gaa acc cat acc tgg cga tcc cag aat gac act gtc acc cca gat gtg	1207
5	Glu Thr His Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val	
	370 375 380	
	tgg tac aca tcc aag cct aaa gaa aaa tta gtc tat gcc att ttt ctt	1255
	Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu	
	385 390 395 400	
10	aaa tgg ccc aca tca gga cag ctg ttc ctt ggc cat ccc aaa gct att	1303
	Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile	
	405 410 415	
	ctg ggg gca aca gag gtg aaa cta ctg ggc cat gga cag cca ctt aac	1351
	Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn	
15	420 425 430	
	tgg att tct ttg gag caa aat ggc att atg gta gaa ctg cca cag cta	1399
	Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu	
	435 440 445	
	acc att cat cag atg ccg tgt aaa tgg ggc tgg gct cta gcc ctg act	1447
20	Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr	
	450 455 460	
	aat gtg atc taaagtgcag cagagtggct gatgctgcaa gttatgtcta aggc	1500
	Asn Val Ile	
	465	
25	taggaactat caggtgtcta taattgtagc acatggagaa agcaaagtga aaactggata	1560
	agaaaattat ttgtgcagtt cagcccttcc cctttttccc actaaatttt ttcttaaatt	1620
	acccatgtaa ccattttaac tctccagtgc actttgccat taaagtctct tcacattg	1678
	<210> 54	
30	<211> 467	
	<212> DNA	
	<213> Homo sapiens	
	<220>	
	<221> CDS	
35	<222> (114)...(413)	

54/177

<400> 54

aggggagggc ggtgctccgc cgcggtggcg gttgctatcg ctctgcagaa cctactcagg 60
 cagccagctg agaagagttg agggaaagtg ctgctgctgg gtctgcagac gcg atg 116

5 Met
 1

gat aac gtg cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg 164
 Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val

5 10 15

10 aaa ggc cac gtg aag atg ctg cgg ctg gat att atc aac tca ctg gta 212
 Lys Gly His Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val

20 25 30

aca aca gta ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa 260
 Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu

15 35 40 45

acc aca aca ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca 308
 Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala

50 55 60 65

gta tgc tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc 356
 Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe

20 70 75 80

aat ccc agc ggt cct tac cag caa aag cct gtg cat gaa aaa aaa gaa 404
 Asn Pro Ser Gly Pro Tyr Gln Gln Lys Pro Val His Glu Lys Lys Glu

85 90 95

25 gtt ttg taattttata ttacttttta gtttgatact aagtattaaa 450
 Val Leu

catatttctg tattctt 467

30 <210> 55
 <211> 875
 <212> DNA
 <213> Homo sapiens
 <220>

35 <221> CDS

55/177

<222> (272)...(841)

<400> 55

	attggttggg ggaaaccac gaggggacgc ggccgaggag ggctgctgtc caccoggggg	60
5	cgtgggagtg aggtaccaga ttcagcccat ttggcccca cgcctctgtt ctoggaatec	120
	gggtgctgcg gattgaggtc ccggttccta acgaatctct gctggattgg ccgtaaccct	180
	gtccccgagc gggctcacag ggtctgaagg ccacgcata ggcaaaggta aagttctgag	240
	ccaccgggtg cctccttccc aggaactgaa g atg gag gaa ggc ggg aac cta	292
	Met Glu Glu Gly Gly Asn Leu	
10	1 5	
	gga ggc ctg att aag atg gtc cat cta ctg gtc ttg tca ggt gcc tgg	340
	Gly Gly Leu Ile Lys Met Val His Leu Leu Val Leu Ser Gly Ala Trp	
	10 15 20	
	ggc atg caa atg tgg gtg acc ttc gtc tca ggc ttc ctg ctt ttc cga	388
15	Gly Met Gln Met Trp Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg	
	25 30 35	
	agc ctt ccc cga cat acc ttc gga cta gtg cag agc aaa ctc ttc ccc	436
	Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys Leu Phe Pro	
	40 45 50 55	
20	ttc tac ttc cac atc tcc atg ggc tgt gcc ttc atc aac ctc tgc atc	484
	Phe Tyr Phe His Ile Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile	
	60 65 70	
	ttg gct tca cag cat gct tgg gct cag ctc aca ttc tgg gag gcc agc	532
	Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser	
25	75 80 85	
	cag ctt tac ctg ctg ttc ctg agc ctt acg ctg gcc act gtc aac gcc	580
	Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala	
	90 95 100	
	cgc tgg ctg gaa ccc cgc acc aca gct gcc atg tgg gcc ctg caa acc	628
30	Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr	
	105 110 115	
	gtg gag aag gag cga ggc ctg ggt ggg gag gta cca ggc agc cac cag	676
	Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln	
	120 125 130 135	
35	ggc ccc gat ccc tac cgc cag ctg cga gag aag gac ccc aag tac agt	724

56/177

Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr Ser
 140 145 150
 gct ctc cgc cag aat ttc ttc cgc tac cat ggg ctg tcc tct ctt tgc 772
 Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser Leu Cys
 5 155 160 165
 aat ctg ggc tgc gtc ctg agc aat ggg ctc tgt ctc gct ggc ctt gcc 820
 Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala Gly Leu Ala
 170 175 180
 ctg gaa ata agg agc ctc tagcatgggc cctgcatgct aataaatgct tcttcag 875
 10 Leu Glu Ile Arg Ser Leu
 185
 <210> 56
 <211> 1256
 15 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (150)...(1241)
 20
 <400> 56
 atgtaagagc cacctcctcc ccaggactca gggatggtc tccagatgtc accactgcag 60
 atattggagc caacactcca gatgctacaa aaggctgtcc agatgtccaa gcttccttgc 120
 cagatgccaa agccaagtcc ccaccgacc atg gtg gac agc ctc ctg gca gtc 173
 25 Met Val Asp Ser Leu Leu Ala Val
 1 5
 acc ctg gct gga aac ctg ggc ctg acc ttc ctc cga ggt tcc cag acc 221
 Thr Leu Ala Gly Asn Leu Gly Leu Thr Phe Leu Arg Gly Ser Gln Thr
 10 15 20
 30 cag agc cat cca gac ctg gga act gag ggc tgc tgg gac cag ctc tct 269
 Gln Ser His Pro Asp Leu Gly Thr Glu Gly Cys Trp Asp Gln Leu Ser
 25 30 35 40
 gcc cct cgg acc ttt acg ctt ttg gac ccc aag gca tct ctg tta acc 317
 Ala Pro Arg Thr Phe Thr Leu Leu Asp Pro Lys Ala Ser Leu Leu Thr
 35 45 50 55

57/177

	aag gcc ttc ctc aat ggc gcc ctg gat ggg gtc atc ctt gga gac tac	365
	Lys Ala Phe Leu Asn Gly Ala Leu Asp Gly Val Ile Leu Gly Asp Tyr	
	60 65 70	
	ctg agc cgg act cct gag ccc cgg cca tcc ctc agc cac ttg ctg agc	413
5	Leu Ser Arg Thr Pro Glu Pro Arg Pro Ser Leu Ser His Leu Leu Ser	
	75 80 85	
	cag tac tat ggg gct ggg gtg gcc aga gac cca ggg ttc cgc agc aac	461
	Gln Tyr Tyr Gly Ala Gly Val Ala Arg Asp Pro Gly Phe Arg Ser Asn	
	90 95 100	
10	ttc cga cgg cag aac ggt gct gct ctg act tca gcc tcc atc ctg gcc	509
	Phe Arg Arg Gln Asn Gly Ala Ala Leu Thr Ser Ala Ser Ile Leu Ala	
	105 110 115 120	
	cag cag gtg tgg gga acc ctt gtc ctt cta cag agg ctg gag cca gta	557
	Gln Gln Val Trp Gly Thr Leu Val Leu Leu Gln Arg Leu Glu Pro Val	
15	125 130 135	
	cac ctc cag ctt cag tgc atg agc caa gaa cag ctg gcc cag gtg gct	605
	His Leu Gln Leu Gln Cys Met Ser Gln Glu Gln Leu Ala Gln Val Ala	
	140 145 150	
	gcc aat gct acc aag gaa ttc act gag gcc ttc ctg gga tgc ccg gcc	653
20	Ala Asn Ala Thr Lys Glu Phe Thr Glu Ala Phe Leu Gly Cys Pro Ala	
	155 160 165	
	atc cac ccc cgc tgc cgc tgg gga gcg gcg cct tat cgg ggc cgc ccg	701
	Ile His Pro Arg Cys Arg Trp Gly Ala Ala Pro Tyr Arg Gly Arg Pro	
	170 175 180	
25	aag ctg ctg cag ctg ccg ctg gga ttc ttg tac gtg cat cac acc tac	749
	Lys Leu Leu Gln Leu Pro Leu Gly Phe Leu Tyr Val His His Thr Tyr	
	185 190 195 200	
	gtg cct gca cca ccc tgc acg gac ttc acg cgc tgc gca gcc aac atg	797
	Val Pro Ala Pro Pro Cys Thr Asp Phe Thr Arg Cys Ala Ala Asn Met	
30	205 210 215	
	cgc tcc atg cag cgc tac cac cag gac acg caa ggc tgg gga gac atc	845
	Arg Ser Met Gln Arg Tyr His Gln Asp Thr Gln Gly Trp Gly Asp Ile	
	220 225 230	
	ggc tac agt ttc gtg gtg ggc tcg gac ggc tac gtg tac gag gga cgc	893
35	Gly Tyr Ser Phe Val Val Gly Ser Asp Gly Tyr Val Tyr Glu Gly Arg	

58/177

	235	240	245	
	ggc tgg cac tgg gtg ggc gcc cac acg ctc ggc cac aac tcc cgg ggc			941
	Gly Trp His Trp Val Gly Ala His Thr Leu Gly His Asn Ser Arg Gly			
	250	255	260	
5	ttc ggc gtg gcc ata gtg ggc aac tac acc gcg gcg ctg ccc acc gag			989
	Phe Gly Val Ala Ile Val Gly Asn Tyr Thr Ala Ala Leu Pro Thr Glu			
	265	270	275	280
	gcc gct ctg cgc acg gtg cgc gac acg ctc ccg agt tgt gcg gtg cgc			1037
	Ala Ala Leu Arg Thr Val Arg Asp Thr Leu Pro Ser Cys Ala Val Arg			
10		285	290	295
	gcc ggc ctc ctg cgg cca gac tac gcg ctg ctg ggc cac cgc cag ctg			1085
	Ala Gly Leu Leu Arg Pro Asp Tyr Ala Leu Leu Gly His Arg Gln Leu			
	300	305	310	
	gtg cgc acc gac tgc ccc ggc gac gcg ctc ttc gac ctg ctg cgc acc			1133
15	Val Arg Thr Asp Cys Pro Gly Asp Ala Leu Phe Asp Leu Leu Arg Thr			
	315	320	325	
	tgg ccg cac ttc acc gcg act gtt aag cca aga cct gcc agg agt gtc			1181
	Trp Pro His Phe Thr Ala Thr Val Lys Pro Arg Pro Ala Arg Ser Val			
	330	335	340	
20	tct aag aga tcc agg agg gag cca ccc cca agg acc ctg cca gcc aca			1229
	Ser Lys Arg Ser Arg Arg Glu Pro Pro Pro Arg Thr Leu Pro Ala Thr			
	345	350	355	360
	gac ctc caa taaagacagc atggaaaac			1256
	Asp Leu Gln			
25				
	<210> 57			
	<211> 884			
	<212> DNA			
	<213> Homo sapiens			
30	<220>			
	<221> CDS			
	<222> (135)...(884)			
	<400> 57			
35	catttccttt ctccacatcc aggtcaggtg gcgtttgctg tggcggctag gcccgcgctgc			60

59/177

	gctggagacc tccgcgtgg ccccgcgag cctcctgcc tggcccggcg ctgcggetct	120
	gccgcggcgg cagc atg ggt ggc ccc cgg ggc gcg ggc tgg gtg gcg gcg	170
	Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala	
	1 5 10	
5	ggc ctg ctg ctc ggc gcg ggc gcc tgc tac tgc att tac agg ctg acc	218
	Gly Leu Leu Leu Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr	
	15 20 25	
	cgg ggt cgg cgg cgg ggc gac cgc gag ctc ggg ata cgc tct tcg aag	266
	Arg Gly Arg Arg Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys	
10	30 35 40	
	tcc gca gaa gac tta act gat ggt tca tat gat gat gtt cta aat gct	314
	Ser Ala Glu Asp Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala	
	45 50 55 60	
	gaa caa ctt cag aaa ctc ctt tac ctg ctg gag tca acg gag gat cct	362
15	Glu Gln Leu Gln Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro	
	65 70 75	
	gta att att gaa aga gct ttg att act ttg ggt aac aat gca gcc ttt	410
	Val Ile Ile Glu Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe	
	80 85 90	
20	tca gtt aac caa gct att att cgt gaa ttg ggt ggt att cca att gtt	458
	Ser Val Asn Gln Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val	
	95 100 105	
	gca aac aaa atc aac cat tcc aac cag agt att aaa gag aaa gct tta	506
	Ala Asn Lys Ile Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu	
25	110 115 120	
	aat gca cta aat aac ctg agt gtg aat gtt gaa aat caa atc aag ata	554
	Asn Ala Leu Asn Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile	
	125 130 135 140	
	aag gtg caa gtt ttg aaa ctg ctt ttg aat ttg tct gaa aat cca gcc	602
30	Lys Val Gln Val Leu Lys Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala	
	145 150 155	
	atg aca gaa gga ctt ctc cgt gcc caa gtg gat tca tca ttc ctt tcc	650
	Met Thr Glu Gly Leu Leu Arg Ala Gln Val Asp Ser Ser Phe Leu Ser	
	160 165 170	
35	ctt tat gac agc cac gta gca aag gag att ctt ctt cga gta ctt acg	698

60/177

	Leu Tyr Asp Ser His Val Ala Lys Glu Ile Leu Leu Arg Val Leu Thr	
	175	180
	cta ttt cag aat ata aag aac tgc ctc aaa ata gaa ggc cat tta gct	746
	Leu Phe Gln Asn Ile Lys Asn Cys Leu Lys Ile Glu Gly His Leu Ala	
5	190	195
	gtg cag cct act ttc act gaa ggt tca ttg ttt ttc ctg tta cat gga	794
	Val Gln Pro Thr Phe Thr Glu Gly Ser Leu Phe Phe Leu Leu His Gly	
	205	210
	gaa gaa tgt gcc cag aaa ata aga gct tta gtt gat cac cat gat gca	842
10	Glu Glu Cys Ala Gln Lys Ile Arg Ala Leu Val Asp His His Asp Ala	
	225	230
	gag gtg aag gaa aag gtt gta aca ata ata ccc aaa atc tga	884
	Glu Val Lys Glu Lys Val Val Thr Ile Ile Pro Lys Ile	
	240	245
15	<210> 58	
	<211> 589	
	<212> DNA	
	<213> Homo sapiens	
20	<220>	
	<221> CDS	
	<222> (48)...(344)	
	<400> 58	
25	gcttttcgag cccgcttgca cctcggcgat ccccgactcc cttcttt atg gcg tcg	56
	Met Ala Ser	
	1	
	ctc ctg tgc tgt ggg ccg aag ctg gcc gcc tgc ggc atc gtc ctc agc	104
	Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile Val Leu Ser	
30	5	10
	gcc tgg gga gtg atc atg ttg ata atg ctc gga ata ttt ttc aat gtc	152
	Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val	
	20	25
	cat tcc gct gtg ttg att gag gac gtt ccc ttc acg gag aaa gat ttt	200
35	His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe	

61/177

	40	45	50	
	gag aat ggc ccc cag aac ata tac aac ctt tac gag caa gtc agc tac			248
	Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu Gln Val Ser Tyr			
	55	60	65	
5	aac tgt ttc atc gct gca ggc ctt tac ctc ctc ctc gga ggc ttc tct			296
	Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly Gly Phe Ser			
	70	75	80	
	ttc tgc caa gtt cgg ctc aat aag cgc aag gaa tac atg gtg cgc			341
	Phe Cys Gln Val Arg Leu Asn Lys Arg Lys Glu Tyr Met Val Arg			
10	85	90	95	
	tagggcccc ggcgcgtttc cccgcctccag cccctcctct atttaaagac tccctgcacc			400
	gtgtcaccoca ggtegcgtcc cacccttgcc ggcgcctct gtgggactgg gtttcccg			460
	cgagagactg aatcccttct cccatctctg gcacccggcc cccgtggaga gggctgaggc			520
	tggggggctg ttccgtctct ccacccttcg ctgtgtcccg tatctcaata aagagaatct			580
15	gtctctcttc			589
	<210> 59			
	<211> 673			
	<212> DNA			
20	<213> Homo sapiens			
	<220>			
	<221> CDS			
	<222> (25)...(543)			
25	<400> 59			
	cttgcccttgc gtgcgcgct cacc atg gtg ggc ccc gcg ccg cgg cgg cgg			51
	Met Val Gly Pro Ala Pro Arg Arg Arg			
	1	5		
	ctg cgg ccg ctg gca gcg ctg gcc ctg gtc ctg gcg ctg gcc ccg ggg			99
30	Leu Arg Pro Leu Ala Ala Leu Ala Leu Val Leu Ala Leu Ala Pro Gly			
	10	15	20	25
	ctg ccc aca gcc cgg gcc ggg cag aca ccg cgc cct gcc gag cgg ggg			147
	Leu Pro Thr Ala Arg Ala Gly Gln Thr Pro Arg Pro Ala Glu Arg Gly			
	30	35	40	
35	ccc cca gtg cgg ctt ttc acc gag gag gag ctg gcc cgc tat ggc ggg			195

62/177

Pro Pro Val Arg Leu Phe Thr Glu Glu Glu Leu Ala Arg Tyr Gly Gly
 45 50 55
 gag gag gaa gat cag ccc atc tac ttg gca gtg aag gga gtg gtg ttt 243
 Glu Glu Glu Asp Gln Pro Ile Tyr Leu Ala Val Lys Gly Val Val Phe
 5 60 65 70
 gat gtc acc tcc gga aag gag ttt tat gga cga gga gcc ccc tac aat 291
 Asp Val Thr Ser Gly Lys Glu Phe Tyr Gly Arg Gly Ala Pro Tyr Asn
 75 80 85
 gcc ttg acg ggg aag gac tcc act aga ggg gta gcc aag atg tcc ttg 339
 10 Ala Leu Thr Gly Lys Asp Ser Thr Arg Gly Val Ala Lys Met Ser Leu
 90 95 100 105
 gat cct gca gac ctc acc cat gac act acg ggt ctc acg gcc aag gaa 387
 Asp Pro Ala Asp Leu Thr His Asp Thr Thr Gly Leu Thr Ala Lys Glu
 110 115 120
 15 ctg gag gcc ctg gat gag gtc ttc acc aaa gtg tac aaa gcc aaa tac 435
 Leu Glu Ala Leu Asp Glu Val Phe Thr Lys Val Tyr Lys Ala Lys Tyr
 125 130 135
 ccc atc gtc ggc tac act gcc cgg aga att ctc aat gag gat ggc agc 483
 Pro Ile Val Gly Tyr Thr Ala Arg Arg Ile Leu Asn Glu Asp Gly Ser
 20 140 145 150
 cct aac ctg gac ttc aag cct gaa gac cag ccc cat ttt gac atc aag 531
 Pro Asn Leu Asp Phe Lys Pro Glu Asp Gln Pro His Phe Asp Ile Lys
 155 160 165
 gat gag ttc tgatgttccc cctgcaggag caggttcttg ggagcgtgag 580
 25 Asp Glu Phe
 170
 gcaggaagac actaggtgct gaatctcctg caaaactggc tgccctggagg ccctgagcca 640
 ccagatctg aataaaacag atgcttacctg tgg 673
 30 <210> 60
 <211> 1425
 <212> DNA
 <213> Homo sapiens
 <220>
 35 <221> CDS

63/177

<222> (127)...(489)

<400> 60

	ccccgcctgg ggcgggtga gtggcaactta agcggggccat gccatgcaac cttgggcgct	60
5	gccaaaccgtg ggcgagctct ggggtgtgagg ggggcctggc ggggcgctcc gctgtgtcag	120
	cgtgtt atg atg ccg tcc cgt acc aac ctg get act gga atc ccc agt	168
	Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser	
	1 5 10	
	agt aaa gtg aaa tat tca agg ctc tcc agc aca gac gat ggc tac att	216
10	Ser Lys Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile	
	15 20 25 30	
	gac ctt cag ttt aag aaa acc cct cct aag atc cct tat aag gcc atc	264
	Asp Leu Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile	
	35 40 45	
15	gca ctt gcc act gtg ctg ttt ttg att ggc gcc ttt ctc att att ata	312
	Ala Leu Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile	
	50 55 60	
	ggc tcc ctc ctg ctg tca ggc tac atc agc aaa ggg ggg gca gac cgg	360
	Gly Ser Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg	
20	65 70 75	
	gcc gtt cca gtg ctg atc att ggc att ctg gtg ttc cta ccc gga ttt	408
	Ala Val Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe	
	80 85 90	
	tac cac ctg cgc atc gct tac tat gca tcc aaa ggc tac cgt ggt tac	456
25	Tyr His Leu Arg Ile Ala Tyr Tyr Ala Ser Lys Gly Tyr Arg Gly Tyr	
	95 100 105 110	
	tcc tat gat gac att cca gac ttt gat gac tagcaccac ccca	500
	Ser Tyr Asp Asp Ile Pro Asp Phe Asp Asp	
	115 120	
30	tagctgagga ggagtcacag tggaaactgtc ccagctttaa gatattctagc agaaactata	560
	gctgaggact aaggaattct gcagcttgca gatgtttaag aaaataatgg ccagattttt	620
	tgggtccttc ccaaagatgt taagtgaacc tacagttagc taattaggac aagctctatt	680
	tttcatccct gggccctgac aagtttttcc acaggaatat gtatcatgga agaatagagg	740
	ttattctgta atggaaaagt gttgcctgcc accaccctct gtagagctga gcatttcttt	800
35	taaatagtct tcattgcca tttgttcttg tagcaaatgg aacaatgtgg tatggcta	860

64/177

ttcttattat taagtagttt attttaaaaa tatctgagta tattatcctg tacacttata 920
 cctaccttca tgttccagtg gaagacctta gtaaaatcaa agatcagtga gttcatctgt 980
 aatatttttt ttacttgctt tcttactgac agcaaccagg aattttttta tctgcagag 1040
 caagttttca aaatgtaaact acttcctctg tttaacagtc cttggaccat tctgatccag 1100
 5 ttcaccagta ggttggacag catataattt gcatcatttt gtcccttgta aatcaagatg 1160
 ttctgcagat tattccttta acggccggac ttttggetgt ttcctaataa aacatgtagt 1220
 gggtattatt tagagtttat agccgtattg ctagcacctt gtagtatgtc atcattctgc 1280
 tcatgattcc aaggatcagc ctggatgcct agaggactag atcaccttag tttgattcta 1340
 ttttttagct tgcaaaaagt gacttatatt ccaaagaaat taaaatgttg aaatccaaat 1400
 10 cctagaaata aaatgagtta acttc 1425

<210> 61

<211> 307

<212> PRT

15 <213> Homo sapiens

<400> 61

Met Ser Met Ile Leu Ser Ala Ser Val Ile Arg Val Arg Asp Gly Leu
 1 5 10 15
 20 Pro Leu Ser Ala Ser Thr Asp Tyr Glu Gln Ser Thr Gly Met Gln Glu
 20 25 30
 Cys Arg Lys Tyr Phe Lys Met Leu Ser Arg Lys Leu Ala Gln Leu Pro
 35 40 45
 Asp Arg Cys Thr Leu Lys Thr Gly His Tyr Asn Ile Asn Phe Ile Ser
 25 50 55 60
 Ser Leu Gly Val Ser Tyr Met Met Leu Cys Thr Glu Asn Tyr Pro Asn
 65 70 75 80
 Val Leu Ala Phe Ser Phe Leu Asp Glu Leu Gln Lys Glu Phe Ile Thr
 85 90 95
 30 Thr Tyr Asn Met Met Lys Thr Asn Thr Ala Val Arg Pro Tyr Cys Phe
 100 105 110
 Ile Glu Phe Asp Asn Phe Ile Gln Arg Thr Lys Gln Arg Tyr Asn Asn
 115 120 125
 Pro Arg Ser Leu Ser Thr Lys Ile Asn Leu Ser Asp Met Gln Thr Glu
 35 130 135 140

65/177

Ile Lys Leu Arg Pro Pro Tyr Gln Ile Ser Met Cys Glu Leu Gly Ser
 145 150 155 160
 Ala Asn Gly Val Thr Ser Ala Phe Ser Val Asp Cys Lys Gly Ala Gly
 165 170 175
 5 Lys Ile Ser Ser Ala His Gln Arg Leu Glu Pro Ala Thr Leu Ser Gly
 180 185 190
 Ile Val Gly Phe Ile Leu Ser Leu Leu Cys Gly Ala Leu Asn Leu Ile
 195 200 205
 Arg Gly Phe His Ala Ile Glu Ser Leu Leu Gln Ser Asp Gly Asp Asp
 10 210 215 220
 Phe Asn Tyr Ile Ile Ala Phe Phe Leu Gly Thr Ala Ala Cys Leu Tyr
 225 230 235 240
 Gln Cys Tyr Leu Leu Val Tyr Tyr Thr Gly Trp Arg Asn Val Lys Ser
 245 250 255
 15 Phe Leu Thr Phe Gly Leu Ile Cys Leu Cys Asn Met Tyr Leu Tyr Glu
 260 265 270
 Leu Arg Asn Leu Trp Gln Leu Phe Phe His Val Thr Val Gly Ala Phe
 275 280 285
 Val Thr Leu Gln Ile Trp Leu Arg Gln Ala Gln Gly Lys Ala Pro Asp
 20 290 295 300
 Tyr Asp Val
 305

 <210> 62
 25 <211> 183
 <212> PRT
 <213> Homo sapiens

 <400> 62
 30 Met Thr Ala Gln Gly Gly Leu Val Ala Asn Arg Gly Arg Arg Phe Lys
 1 5 10 15
 Trp Ala Ile Glu Leu Ser Gly Pro Gly Gly Gly Ser Arg Gly Arg Ser
 20 25 30
 Asp Arg Gly Ser Gly Gln Gly Asp Ser Leu Tyr Pro Val Gly Tyr Leu
 35 35 40 45

66/177

Asp Lys Gln Val Pro Asp Thr Ser Val Gln Glu Thr Asp Arg Ile Leu
 50 55 60
 Val Glu Lys Arg Cys Trp Asp Ile Ala Leu Gly Pro Leu Lys Gln Ile
 65 70 75 80
 5 Pro Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr Ile Ser Ile
 85 90 95
 Phe Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro Ile Gln Ala
 100 105 110
 Leu Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln
 10 115 120 125
 Lys Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu
 130 135 140
 Ala Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His
 145 150 155 160
 15 Ala Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg Met Glu Phe
 165 170 175
 Ser Gly Gly Gly Leu Leu Leu
 180
 20 <210> 63
 <211> 327
 <212> PRT
 <213> Homo sapiens
 25 <400> 63
 Met Arg Ala Leu Pro Gly Leu Leu Glu Ala Arg Ala Arg Thr Pro Arg
 1 5 10 15
 Leu Leu Leu Leu Gln Cys Leu Leu Ala Ala Ala Arg Pro Ser Ser Ala
 20 25 30
 30 Asp Gly Ser Ala Pro Asp Ser Pro Phe Thr Ser Pro Pro Leu Arg Glu
 35 40 45
 Glu Ile Met Ala Asn Asn Phe Ser Leu Glu Ser His Asn Ile Ser Leu
 50 55 60
 Thr Glu His Ser Ser Met Pro Val Glu Lys Asn Ile Thr Leu Glu Arg
 35 65 70 75 80

67/177

Pro Ser Asn Val Asn Leu Thr Cys Gln Phe Thr Thr Ser Gly Asp Leu
 85 90 95
 Asn Ala Val Asn Val Thr Trp Lys Lys Asp Gly Glu Gln Leu Glu Asn
 100 105 110
 5 Asn Tyr Leu Val Ser Ala Thr Gly Ser Thr Leu Tyr Thr Gln Tyr Arg
 115 120 125
 Phe Thr Ile Ile Asn Ser Lys Gln Met Gly Ser Tyr Ser Cys Phe Phe
 130 135 140
 Arg Glu Glu Lys Glu Gln Arg Gly Thr Phe Asn Phe Lys Val Pro Glu
 10 145 150 155 160
 Leu His Gly Lys Asn Lys Pro Leu Ile Ser Tyr Val Gly Asp Ser Thr
 165 170 175
 Val Leu Thr Cys Lys Cys Gln Asn Cys Phe Pro Leu Asn Trp Thr Trp
 180 185 190
 15 Tyr Ser Ser Asn Gly Ser Val Lys Val Pro Val Gly Val Gln Met Asn
 195 200 205
 Lys Tyr Val Ile Asn Gly Thr Tyr Ala Asn Glu Thr Lys Leu Lys Ile
 210 215 220
 Thr Gln Leu Leu Glu Glu Asp Gly Glu Ser Tyr Trp Cys Arg Ala Leu
 20 225 230 235 240
 Phe Gln Leu Gly Glu Ser Glu Glu His Ile Glu Leu Val Val Leu Ser
 245 250 255
 Tyr Leu Val Pro Leu Lys Pro Phe Leu Val Ile Val Ala Glu Val Ile
 260 265 270
 25 Leu Leu Val Ala Thr Ile Leu Leu Cys Glu Lys Tyr Thr Gln Lys Lys
 275 280 285
 Lys Lys His Ser Asp Glu Gly Lys Glu Phe Glu Gln Ile Glu Gln Leu
 290 295 300
 Lys Ser Asp Asp Ser Asn Gly Ile Glu Asn Asn Val Pro Arg His Arg
 30 305 310 315 320
 Lys Asn Glu Ser Leu Gly Gln
 325

<210> 64

35 <211> 223

68/177

<212> PRT

<213> Homo sapiens

<400> 64

5 Met Lys Phe Val Pro Cys Leu Leu Leu Val Thr Leu Ser Cys Leu Gly
 1 5 10 15
 Thr Leu Gly Gln Ala Pro Arg Gln Lys Gln Gly Ser Thr Gly Glu Glu
 20 25 30
 Phe His Phe Gln Thr Gly Gly Arg Asp Ser Cys Thr Met Arg Pro Ser
 10 35 40 45
 Ser Leu Gly Gln Gly Ala Gly Glu Val Trp Leu Arg Val Asp Cys Arg
 50 55 60
 Asn Thr Asp Gln Thr Tyr Trp Cys Glu Tyr Arg Gly Gln Pro Ser Met
 65 70 75 80
 15 Cys Gln Ala Phe Ala Ala Asp Pro Lys Ser Tyr Trp Asn Gln Ala Leu
 85 90 95
 Gln Glu Leu Arg Arg Leu His His Ala Cys Gln Gly Ala Pro Val Leu
 100 105 110
 Arg Pro Ser Val Cys Arg Glu Ala Gly Pro Gln Ala His Met Gln Gln
 20 115 120 125
 Val Thr Ser Ser Leu Lys Gly Ser Pro Glu Pro Asn Gln Gln Pro Glu
 130 135 140
 Ala Gly Thr Pro Ser Leu Arg Pro Lys Ala Thr Val Lys Leu Thr Glu
 145 150 155 160
 25 Ala Thr Gln Leu Gly Lys Asp Ser Met Glu Glu Leu Gly Lys Ala Lys
 165 170 175
 Pro Thr Thr Arg Pro Thr Ala Lys Pro Thr Gln Pro Gly Pro Arg Pro
 180 185 190
 Gly Gly Asn Glu Glu Ala Lys Lys Lys Ala Trp Glu His Cys Trp Lys
 30 195 200 205
 Pro Phe Gln Ala Leu Cys Ala Phe Leu Ile Ser Phe Phe Arg Gly
 210 215 220

<210> 65

35 <211> 48

69/177

<212> PRT

<213> Homo sapiens

<400> 65

5 Met Arg Leu Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg
1 5 10 15
Ser Glu Ala Ser Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys
20 25 30
10 Met Gln Tyr Ala Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser
35 40 45

<210> 66

<211> 371

<212> PRT

15 <213> Homo sapiens

<400> 66

Met Ala Trp Thr Lys Tyr Gln Leu Phe Leu Ala Gly Leu Met Leu Val
1 5 10 15
20 Thr Gly Ser Ile Asn Thr Leu Ser Ala Lys Trp Ala Asp Asn Phe Met
20 25 30
Ala Glu Gly Cys Gly Gly Ser Lys Glu His Ser Phe Gln His Pro Phe
35 40 45
Leu Gln Ala Val Gly Met Phe Leu Gly Glu Phe Ser Cys Leu Ala Ala
25 50 55 60
Phe Tyr Leu Leu Arg Cys Arg Ala Ala Gly Gln Ser Asp Ser Ser Val
65 70 75 80
Asp Pro Gln Gln Pro Phe Asn Pro Leu Leu Phe Leu Pro Pro Ala Leu
85 90 95
30 Cys Asp Met Thr Gly Thr Ser Leu Met Tyr Val Ala Leu Asn Met Thr
100 105 110
Ser Ala Ser Ser Phe Gln Met Leu Arg Gly Ala Val Ile Ile Phe Thr
115 120 125
Gly Leu Phe Ser Val Ala Phe Leu Gly Arg Arg Leu Val Leu Ser Gln
35 130 135 140

70/177

Trp Leu Gly Ile Leu Ala Thr Ile Ala Gly Leu Val Val Val Gly Leu
 145 150 155 160
 Ala Asp Leu Leu Ser Lys His Asp Ser Gln His Lys Leu Ser Glu Val
 165 170 175
 5 Ile Thr Gly Asp Leu Leu Ile Ile Met Ala Gln Ile Ile Val Ala Ile
 180 185 190
 Gln Met Val Leu Glu Glu Lys Phe Val Tyr Lys His Asn Val His Pro
 195 200 205
 Leu Arg Ala Val Gly Thr Glu Gly Leu Phe Gly Phe Val Ile Leu Ser
 10 210 215 220
 Leu Leu Leu Val Pro Met Tyr Tyr Ile Pro Ala Gly Ser Phe Ser Gly
 225 230 235 240
 Asn Pro Arg Gly Thr Leu Glu Asp Ala Leu Asp Ala Phe Cys Gln Val
 245 250 255
 15 Gly Gln Gln Pro Leu Ile Ala Val Ala Leu Leu Gly Asn Ile Ser Ser
 260 265 270
 Ile Ala Phe Phe Asn Phe Ala Gly Ile Ser Val Thr Lys Glu Leu Ser
 275 280 285
 Ala Thr Thr Arg Met Val Leu Asp Ser Leu Arg Thr Val Val Ile Trp
 20 290 295 300
 Ala Leu Ser Leu Ala Leu Gly Trp Glu Ala Phe His Ala Leu Gln Ile
 305 310 315 320
 Leu Gly Phe Leu Ile Leu Leu Ile Gly Thr Ala Leu Tyr Asn Gly Leu
 325 330 335
 25 His Arg Pro Leu Leu Gly Arg Leu Ser Arg Gly Arg Pro Leu Ala Glu
 340 345 350
 Glu Ser Glu Gln Glu Arg Leu Leu Gly Gly Thr Arg Thr Pro Ile Asn
 355 360 365
 Asp Ala Ser
 30 370

 <210> 67
 <211> 90
 <212> PRT
 35 <213> Homo sapiens

71/177

<400> 67

Met Phe His Gln Ile Trp Ala Ala Leu Leu Tyr Phe Tyr Gly Ile Ile
 1 5 10 15
 5 Leu Asn Ser Ile Tyr Gln Cys Pro Glu His Ser Gln Leu Thr Thr Leu
 20 25 30
 Gly Val Asp Gly Lys Glu Phe Pro Glu Val His Leu Gly Gln Trp Tyr
 35 40 45
 Phe Ile Ala Gly Ala Ala Pro Thr Lys Glu Glu Leu Ala Thr Phe Asp
 10 50 55 60
 Pro Val Asp Asn Ile Val Phe Asn Met Ala Ala Gly Ser Ala Pro Met
 65 70 75 80
 Gln Leu His Leu Arg Ala Thr Ile Arg Met
 85 90

15

<210> 68

<211> 499

<212> PRT

<213> Homo sapiens

20

<400> 68

Met Val Asp Arg Gly Pro Leu Leu Thr Ser Ala Ile Ile Phe Tyr Leu
 1 5 10 15
 Ala Ile Gly Ala Ala Ile Phe Glu Val Leu Glu Glu Pro His Trp Lys
 25 20 25 30
 Glu Ala Lys Lys Asn Tyr Tyr Thr Gln Lys Leu His Leu Leu Lys Glu
 35 40 45
 Phe Pro Cys Leu Gly Gln Glu Gly Leu Asp Lys Ile Leu Glu Val Val
 50 55 60
 30 Ser Asp Ala Ala Gly Gln Gly Val Ala Ile Thr Gly Asn Gln Thr Phe
 65 70 75 80
 Asn Asn Trp Asn Trp Pro Asn Ala Met Ile Phe Ala Ala Thr Val Ile
 85 90 95
 Thr Thr Ile Gly Tyr Gly Asn Val Ala Pro Lys Thr Pro Ala Gly Arg
 35 100 105 110

72/177

Leu Phe Cys Val Phe Tyr Gly Leu Phe Gly Val Pro Leu Cys Leu Thr
 115 120 125
 Trp Ile Ser Ala Leu Gly Lys Phe Phe Gly Gly Arg Ala Lys Arg Leu
 130 135 140
 5 Gly Gln Phe Leu Thr Lys Arg Gly Val Ser Leu Arg Lys Ala Gln Ile
 145 150 155 160
 Thr Cys Thr Val Ile Phe Ile Val Trp Gly Val Leu Val His Leu Val
 165 170 175
 Ile Pro Pro Phe Val Phe Met Val Thr Glu Gly Trp Asn Tyr Ile Glu
 10 180 185 190
 Gly Leu Tyr Tyr Ser Phe Ile Thr Ile Ser Thr Ile Gly Phe Gly Asp
 195 200 205
 Phe Val Ala Gly Val Asn Pro Ser Ala Asn Tyr His Ala Leu Tyr Arg
 210 215 220
 15 Tyr Phe Val Glu Leu Trp Ile Tyr Leu Gly Leu Ala Trp Leu Ser Leu
 225 230 235 240
 Phe Val Asn Trp Lys Val Ser Met Phe Val Glu Val His Lys Ala Ile
 245 250 255
 Lys Lys Arg Arg Arg Arg Arg Lys Glu Ser Phe Glu Ser Ser Pro His
 20 260 265 270
 Ser Arg Lys Ala Leu Gln Val Lys Gly Ser Thr Ala Ser Lys Asp Val
 275 280 285
 Asn Ile Phe Ser Phe Leu Ser Lys Lys Glu Glu Thr Tyr Asn Asp Leu
 290 295 300
 25 Ile Lys Gln Ile Gly Lys Lys Ala Met Lys Thr Ser Gly Gly Gly Glu
 305 310 315 320
 Thr Gly Pro Gly Pro Gly Leu Gly Pro Gln Gly Gly Gly Leu Pro Ala
 325 330 335
 Leu Pro Pro Ser Leu Val Pro Leu Val Val Tyr Ser Lys Asn Arg Val
 30 340 345 350
 Pro Thr Leu Glu Glu Val Ser Gln Thr Leu Arg Ser Lys Gly His Val
 355 360 365
 Ser Arg Ser Pro Asp Glu Glu Ala Val Ala Arg Ala Pro Glu Asp Ser
 370 375 380
 35 Ser Pro Ala Pro Glu Val Phe Met Asn Gln Leu Asp Arg Ile Ser Glu

73/177

385 390 395 400
 Glu Cys Glu Pro Trp Asp Ala Gln Asp Tyr His Pro Leu Ile Phe Gln
 405 410 415
 Asp Ala Ser Ile Thr Phe Val Asn Thr Glu Ala Gly Leu Ser Asp Glu
 5 420 425 430
 Glu Thr Ser Lys Ser Ser Leu Glu Asp Asn Leu Ala Gly Glu Glu Ser
 435 440 445
 Pro Gln Gln Gly Ala Glu Ala Lys Ala Pro Leu Asn Met Gly Glu Phe
 450 455 460
 10 Pro Ser Ser Ser Glu Ser Thr Phe Thr Ser Thr Glu Ser Glu Leu Ser
 465 470 475 480
 Val Pro Tyr Glu Gln Leu Met Asn Glu Tyr Asn Lys Ala Asn Ser Pro
 485 490 495
 Lys Gly Thr
 15

 <210> 69
 <211> 106
 <212> PRT
 20 <213> Homo sapiens

 <400> 69
 Met Ala Ser Ser Gly Ala Gly Asp Pro Leu Asp Ser Lys Arg Gly Glu
 1 5 10 15
 25 Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr Arg Glu Lys Leu Thr Pro
 20 25 30
 Glu Gln Leu His Ser Met Arg Gln Ala Glu Leu Ala Gln Trp Gln Lys
 35 40 45
 Val Leu Pro Arg Arg Arg Thr Arg Asn Ile Val Thr Gly Leu Gly Ile
 30 50 55 60
 Gly Ala Leu Val Leu Ala Ile Tyr Gly Tyr Thr Phe Tyr Ser Ile Ser
 65 70 75 80
 Gln Glu Arg Phe Leu Asp Glu Leu Glu Asp Glu Ala Lys Ala Ala Arg
 85 90 95
 35 Ala Arg Ala Leu Ala Arg Ala Ser Gly Ser

74/177

100

105

<210> 70

<211> 152

5 <212> PRT

<213> Homo sapiens

<400> 70

10 Met Asp Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp
 1 5 10 15
 Glu Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu
 20 25 30
 Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly Ile
 35 40 45
 15 Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp Lys Lys
 50 55 60
 Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly Arg Pro Glu
 65 70 75 80
 Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His Glu Asp Ala Leu
 85 90 95
 20 Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe Pro Asp Val Ser Gly
 100 105 110
 Val Ser Arg Ile Pro Ser Arg Ser Val Pro Ala Ser Asp Cys Val Ser
 115 120 125
 25 Gly Gln Asp Leu His Ser Thr Val Tyr Glu Val Ile Gln His Ile Pro
 130 135 140
 Ala Gln Gln Gln Asp His Pro Glu
 145 150

30 <210> 71

<211> 921

<212> DNA

<213> Homo sapiens

35 <400> 71

75/177

atgtctatga ttttatctgc ctcaagtcatt cgtgtcagag atggactgcc actttctget 60
 tctactgatt atgaacaaaag cacaggaatg caggagtgc gaaagtattt taaaatgctt 120
 tcgaggaaac ttgctcaact tcctgataga tgtacactga aaactggaca ttataacatt 180
 aattttatta gctctctggg agtgagctac atgatgttgt gcaactgaaaa ttacccaaat 240
 5 gttctcgccct tctctttcct ggatgagctt cagaaggagt tcattactac ttataacatg 300
 atgaagacaa ataactgctgt cagaccatac tgtttcattg aatttgataa cttoattcag 360
 aggaccaagc agcgatataa taatcccagg tctctttcaa caaagataaa tctttctgac 420
 atgcagacgg aaatcaagct gaggcctcct tatcaaattt ccatgtgcga actgggggtca 480
 gccaatggag tcacatcagc attttctgtt gactgtaaag gtgctggtaa gattttcttct 540
 10 gctcaccagc gactggaacc agcaactctg tcagggattg taggatttat ccttagtctt 600
 ttatgtggag ctctgaattt aattcgaggc tttcatgcta tagaaagtct cctgcagagt 660
 gatggtgatg attttaatta catcattgca tttttccttg gaacagcagc ctgcctttac 720
 cagtgttatt tacttgtcta ctacaccggc tggcggaatg tcaaactctt tttgactttt 780
 ggcttaatat gtctatgcaa catgtatctc tatgaactgc gcaacctctg gcagcttttc 840
 15 tttcatgtga ctgtgggagc atttgttaca ctacagatct ggctaaggca agcccagggc 900
 aaggetcccg attatgatgt c 921

<210> 72

<211> 549

20 <212> DNA

<213> Homo sapiens

<400> 72

atgacggccc aggggggcct ggtggctaac cgaggccggc gcttcaagtg ggccattgag 60
 25 ctaagcgggc ctggaggagg cagcaggggt cgaagtgacc ggggcagtgg ccaggagagc 120
 tcgctctacc cagtcgggta cttggacaag caagtgcctg ataccagcgt gcaagagaca 180
 gaccggatcc tgggtggagaa gcgctgctgg gacatcgccct tgggtcccct caaacagatt 240
 cccatgaatc tcttcacat gtacatggca ggcaatacta tctccatctt cctactatg 300
 atggtgtgta tgatggcctg gcgacccatt caggcaactta tggccatttc agccacttcc 360
 30 aagatgttag aaagttcaag ccagaagttt cttcagggtt tgggtctatct cattgggaac 420
 ctgatgggtt tggcattggc tgtttacaag tgccagtcca tgggactgtt acctacacat 480
 gcatcggatt gggttagcctt cattgagccc cctgagagaa tggagtccag tgggtggagga 540
 ctgcttttg 549

35 <210> 73

76/177

<211> 981

<212> DNA

<213> Homo sapiens

5

<400> 73

	atgcgcgccc	tccccggcct	gctggaggcc	agggcgcgta	cgccccggct	gctcctcctc	60
	cagtgccttc	tcgctgccgc	gcgcccgaagc	tcggcggacg	gcagtgcctc	agattcgctt	120
	tttacaagtc	cacctctcag	agaagaaata	atggcaaata	acttttcctt	ggagagtcct	180
	aacatatcac	tgactgaaca	ttctagtatg	ccagtagaaa	aaaatatcac	tttagaaagg	240
10	cctttctaatg	ttaaattcac	atgccagttc	acaacatctg	gggatttgaa	tgcagtaaag	300
	gtgacttgga	aaaaagatgg	tgaacaactt	gagaataatt	atcttgctag	tgcaacagga	360
	agcaccttgt	ataccaata	caggttcacc	atcattaata	gcaaacaagt	gggaagttat	420
	tcttgcttct	ttcgagagga	aaaggaacaa	aggggaacat	ttaatttcaa	agtccctgaa	480
	cttcattgga	aaaacaagcc	attgatctct	tacgtagggg	attctactgt	cttgacatgt	540
15	aaatgtcaaa	attgttttcc	tttaaattgg	acctggtaca	gtagtaattg	gagtgtaaag	600
	gttcctgttg	gtgttcaaat	gaataaatat	gtgatcaatg	gaacatatgc	taacgaaaca	660
	aagctgaaga	taacacaact	tttgaggaga	gatggggaat	cttactggtg	ccgtgcacta	720
	ttccaattag	gcgagagtga	agaacacatt	gagcttggtg	tgctgagcta	tttggtgccc	780
	ctcaaaccat	ttcttgtaat	agtggctgag	gtgattcttt	tagtgccac	cattctgctt	840
20	tgtgaaaagt	acacacaaaa	gaaaaagaag	cactcagatg	aggggaaaga	atttgagcag	900
	attgaacagc	tgaaatcaga	tgatagcaat	ggtatagaaa	ataatgtccc	caggcataga	960
	aaaaatgagt	ctctgggcca	g				981

<210> 74

25

<211> 669

<212> DNA

<213> Homo sapiens

<400> 74

30

	atgaagtctg	tcccttgcct	cctgctggtg	accttgctct	gcctggggac	tttgggtcag	60
	gccccgaggg	aaaagcaagg	aagcactggg	gaggaaattc	atttccagac	tggagggaga	120
	gattcctgca	ctatgcgtcc	cagcagcttg	gggcaagggt	ctggagaagt	ctggcttcgc	180
	gtcgactgcc	gcaacacaga	ccagacctac	tggtgtgagt	acagggggca	gccagcagtg	240
	tgccaggett	tcgctgctga	ccccaaatct	tactggaatc	aagccctgca	ggagctgagg	300
35	cgccttcacc	atgcgtgcc	ggggggcccc	gtgcttaggc	catccgtgtg	cagggaggct	360

77/177

	ggaccccagg cccatatgca gcaggtgact tccagcctca agggcagccc agagcccaac	420
	cagcagcctg aggctgggac gccatctctg agggccaagg ccacagtga actcacagaa	480
	gcaacacagc tgggaaagga ctogatggaa gagctgggaa aagccaaacc caccaccoga	540
	cccacagcca aacctaccca gcctggaccc agggccggag ggaatgagga agcaaagaag	600
5	aaggcctggg aacattgttg gaaacccttc caggccctgt gcgcctttct catcagcttc	660
	ttccgaggg	669
	<210> 75	
	<211> 144	
10	<212> DNA	
	<213> Homo sapiens	
	<400> 75	
	atgaggettc tgctgcttct cctagtggcg gcgtctgcga tggtcggag cgaggcctcg	60
15	gccaatctgg gcggcgtgcc cagcaagaga ttaaagatgc agtacgccac ggggcccgtg	120
	ctcaagttec agatttgtgt ttec	144
	<210> 76	
	<211> 1113	
20	<212> DNA	
	<213> Homo sapiens	
	<400> 76	
	atggcctgga ccaagtacca gctgttctct gccgggctca tgcttggttac cggctccatc	60
25	aacacgctct cggcaaaatg ggccggacaat ttcattggcg agggctgtgg agggagcaag	120
	gagcacagct tccagcatcc ctctctccag gcagtgggca tgttctctggg agaattctcc	180
	tgcttggtct ccttctacct cctccgatgc agagctgcag ggcaatcaga ctccagcgta	240
	gacccccagc agcccttcaa ccctcttctt ttcttgcccc cagcgtctct tgacatgaca	300
	gggaccagcc tcatgtatgt ggctctgaac atgaccagt cctccagctt ccagatgctg	360
30	cgggggtgcag tgatcatatt cactggcctg ttctcggtgg ccttctctggg ccggaggctg	420
	gtgctgagcc agtggctggg catcctagcc accatcgagg ggctgggtgg cgtgggcctg	480
	gctgacctcc tgagcaagca cgacagtcag cacaagctca gcgaagtgat cacaggggac	540
	ctgttgatca tcatggccca gatcctcgtt gccatccaga tgggtgctaga ggagaagttc	600
	gtctacaaac acaatgtgca cccactgagg gcagttggca ctgagggcct ctttggtctt	660
35	gtgatcctct ccctgctgct ggtgcccatt tactacatcc ccgcggctc cttcagcgga	720

78/177

	aaccctcgtg ggacaactgga ggatgcattg gacgccttct gccaggtggg ccagcagcgg	780
	ctcattgccg tggcactgct gggcaacatc agcagcattg ccttcttcaa cttegcaggg	840
	atcagcgtca ccaaggaact gagcgccacc acccgcatgg tgttggacag cttgcgcacc	900
	gttgtcatct gggcactgag cctggcactg ggctgggagg ccttccatgc actgcagatc	960
5	cttggtcttc tcatactect tataggcact gccctctaca atgggctaca ccgtccgctg	1020
	ctgggcccgc tgtccagggg ccggcccctg gcagaggaga gcgagcagga gagactgctg	1080
	ggtggcaccg gcactcccat caatgatgcc agc	1113
	<210> 77	
10	<211> 270	
	<212> DNA	
	<213> Homo sapiens	
	<400> 77	
15	atgttccacc aaatttgggc agctctgctc tacttctatg gtattatcct taactccatc	60
	taccagtgcc ctgagcacag tcaactgaca actctgggcg tggatgggaa ggagttecca	120
	gaggteccact tgggcccagtg gtactttatc gcaggggcag ctcccaccaa ggaggagtgtg	180
	gcaacttttg accctgtgga caacattgtc ttcaatatgg ctgctggctc tgccccgatg	240
	cagctccacc ttcgtgctac catccgatg	270
20	<210> 78	
	<211> 1497	
	<212> DNA	
	<213> Homo sapiens	
25	<400> 78	
	atggtggacc gggggccctct gctcacctcg gccatcatct ttacactggc catcggggcg	60
	gcgatcttcg aagtgtctgga ggagccacac tggaggagg ccaagaaaa ctactacaca	120
	cagaagctgc atctgtctaa ggagtteccg tgctgggtc aggaggcct ggacaagatc	180
30	ctagagggtgg tatctgatgc tgcaggacag ggtgtggcca tcacaggga ccagaccttc	240
	aacaactgga actggcccaa tgcaatgatt tttgcagcga ccgtcattac caccattgga	300
	tatggcaatg tggtcccaa gacccccgcg ggtgcctct tctgtgtttt ctatggtctc	360
	ttcgggggtgc cgtctctgct gacgtggatc agtgccttg gcaagttctt cgggggacgt	420
	gccaaagagac tagggcagtt ccttaccag agagggtgtga gtctgcggaa ggcgcagatc	480
35	acgtgcacag tcattctcat cgtgtggggc gtctagtcc acctggtgat cccacccttc	540

79/177

gtattcatgg tgactgaggg gtggaactac atcgagggcc tctactactc cttcatcacc 600
 atctccacca tcggcttcgg tgactttgtg gccggtgtga accccagcgc caactaccac 660
 gccctgtacc gctacttcgt ggagctctgg atctacttgg ggctggcctg gctgtccctt 720
 tttgtcaact ggaaggtgag catgtttgtg gaagtccaca aagccattaa gaagcggcgg 780
 5 cggcgacgga aggagtcctt tgagagctcc ccacactccc ggaaggccct gcaggtgaag 840
 gggagcacag cctccaagga cgtcaacatc ttcagctttc tttccaagaa ggaagagacc 900
 tacaacgacc tcatcaagca gatcgggaag aaggccatga agacaagcgg ggggtggggag 960
 acggggcccg gcccgaggct ggggcctcaa ggcggtgggc tcccagcact gccccttcc 1020
 ctggtgcccc tggtagtcta ctccaagaac cgggtgcccc ccttggaaga ggtgtcacag 1080
 10 aactgagga gcaaaggcca cgtatcaagg tcccagatg aggaggctgt ggcacgggcc 1140
 cctgaagaca gctccccctgc ccccgagggtg ttcatgaacc agctggaccg catcagcgag 1200
 gaatgcgagc catgggacgc ccaggactac caccactca tcttccagga cgcagcctc 1260
 accttcgtga acacggaggc tggcctctca gacgaggaga cctccaagtc ctgcgtagag 1320
 gacaacttgg caggggagga gagccccag cagggggctg aagccaaggc gcccctgaac 1380
 15 atgggcgagt tcccctctc ctccagctcc accttcacca gcaactgagtc tgagctctct 1440
 gtgccttacg aacagctgat gaatgagtag aacaaggcta acagcccaa gggcaca 1497

<210> 79

<211> 318

20 <212> DNA

<213> Homo sapiens

<400> 79

atggcgtctt cgggagctgg tgacctctg gattctaagc gtggagaggg cccgttcgct 60
 25 cagcgtatcg acccgactcg ggagaagctg acaccgagc aactgcattc catgcggcag 120
 gcggagcttg cccagtgga gaaggtccta ccacggcggc gaaccgggaa catcgtgacc 180
 ggcctaggca tcggggccct ggtgttggt atttatggtt acaccttcta ctgatttcc 240
 caggagcgtt tctagatga gctagaagac gaggccaaag ctgcccagc ccgagctctg 300
 gcaagggcgt cagggtcc 318

30

<210> 80

<211> 456

<212> DNA

<213> Homo sapiens

35

80/177

<400> 80

atggactatg tgtgctgtgc ttacaacaac ataaccggca ggcaagatga aactcatttc 60

acagttatca tcaactccgt aggactggag aagcttgac agaaaggaaa atcattgtca 120

ccttttagcaa gtataactgg aatatcacta tttttgatta tatccatgtg tcttctcttc 180

5 ctatggaaaa aatatcaacc ctacaaagt ataaaacaga aactagaagg caggccagaa 240

acagaataca ggaaagctca aacattttca ggccatgaag atgctctgga tgacttcgga 300

atatatgaat ttgttgcttt tccagatgtt tctggtgttt ccaggatccc aagcaggtct 360

gttccagcct ctgatttgt atcggggcaa gatttgaca gtacagtga tgaagttatt 420

cagcacatcc ctgcccagca gcaagaccat ccagag 456

10

<210> 81

<211> 1436

<212> DNA

<213> Homo sapiens

15 <220>

<221> CDS

<222> (66)...(989)

<400> 81

20 gcacttcggg gcgcgtcact cggagcggcg ggtcccgtct cgacaggtct tctctgttgg 60

ttgaa atg tct atg att tta tct gcc tca gtc att cgt gtc aga gat 107

Met Ser Met Ile Leu Ser Ala Ser Val Ile Arg Val Arg Asp

1 5 10

gga ctg cca ctt tct gct tct act gat tat gaa caa agc aca gga atg 155

25 Gly Leu Pro Leu Ser Ala Ser Thr Asp Tyr Glu Gln Ser Thr Gly Met

15 20 25 30

cag gag tgc aga aag tat ttt aaa atg ctt tcg agg aaa ctt gct caa 203

Gln Glu Cys Arg Lys Tyr Phe Lys Met Leu Ser Arg Lys Leu Ala Gln

35 40 45

30 ctt cct gat aga tgt aca ctg aaa act gga cat tat aac att aat ttt 251

Leu Pro Asp Arg Cys Thr Leu Lys Thr Gly His Tyr Asn Ile Asn Phe

50 55 60

att agc tct ctg gga gtg agc tac atg atg ttg tgc act gaa aat tac 299

Ile Ser Ser Leu Gly Val Ser Tyr Met Met Leu Cys Thr Glu Asn Tyr

35 65 70 75

81/177

	cca aat gtt ctc gcc ttc tct ttc ctg gat gag ctt cag aag gag ttc	347
	Pro Asn Val Leu Ala Phe Ser Phe Leu Asp Glu Leu Gln Lys Glu Phe	
	80 85 90	
	att act act tat aac atg atg aag aca aat act gct gtc aga cca tac	395
5	Ile Thr Thr Tyr Asn Met Met Lys Thr Asn Thr Ala Val Arg Pro Tyr	
	95 100 105 110	
	tgt ttc att gaa ttt gat aac ttc att cag agg acc aag cag cga tat	443
	Cys Phe Ile Glu Phe Asp Asn Phe Ile Gln Arg Thr Lys Gln Arg Tyr	
	115 120 125	
10	aat aat ccc agg tct ctt tca aca aag ata aat ctt tct gac atg cag	491
	Asn Asn Pro Arg Ser Leu Ser Thr Lys Ile Asn Leu Ser Asp Met Gln	
	130 135 140	
	acg gaa atc aag ctg agg cct cct tat caa att tcc atg tgc gaa ctg	539
	Thr Glu Ile Lys Leu Arg Pro Pro Tyr Gln Ile Ser Met Cys Glu Leu	
15	145 150 155	
	ggg tca gcc aat gga gtc aca tca gca ttt tct gtt gac tgt aaa ggt	587
	Gly Ser Ala Asn Gly Val Thr Ser Ala Phe Ser Val Asp Cys Lys Gly	
	160 165 170	
	gct ggt aag att tct tct gct cac cag cga ctg gaa cca gca act ctg	635
20	Ala Gly Lys Ile Ser Ser Ala His Gln Arg Leu Glu Pro Ala Thr Leu	
	175 180 185 190	
	tca ggg att gta gga ttt atc ctt agt ctt tta tgt gga gct ctg aat	683
	Ser Gly Ile Val Gly Phe Ile Leu Ser Leu Leu Cys Gly Ala Leu Asn	
	195 200 205	
25	tta att cga ggc ttt cat gct ata gaa agt ctc ctg cag agt gat ggt	731
	Leu Ile Arg Gly Phe His Ala Ile Glu Ser Leu Leu Gln Ser Asp Gly	
	210 215 220	
	gat gat ttt aat tac atc att gca ttt ttc ctt gga aca gca gcc tgc	779
	Asp Asp Phe Asn Tyr Ile Ile Ala Phe Phe Leu Gly Thr Ala Ala Cys	
30	225 230 235	
	ctt tac cag tgt tat tta ctt gtc tac tac acc ggc tgg cgg aat gtc	827
	Leu Tyr Gln Cys Tyr Leu Leu Val Tyr Tyr Thr Gly Trp Arg Asn Val	
	240 245 250	
	aaa tct ttt ttg act ttt ggc tta atc tgt cta tgc aac atg tat ctc	875
35	Lys Ser Phe Leu Thr Phe Gly Leu Ile Cys Leu Cys Asn Met Tyr Leu	

82/177

	255	260	265	270	
	tat gaa ctg cgc aac ctc tgg cag ctt ttc ttt cat gtg act gtg gga				923
	Tyr Glu Leu Arg Asn Leu Trp Gln Leu Phe Phe His Val Thr Val Gly				
		275	280	285	
5	gca ttt gtt aca cta cag atc tgg cta agg caa gcc cag ggc aag gct				971
	Ala Phe Val Thr Leu Gln Ile Trp Leu Arg Gln Ala Gln Gly Lys Ala				
		290	295	300	
	ccc gat tat gat gtc tgacaccatc cttcagatct attgccttgg ctte				1020
	Pro Asp Tyr Asp Val				
10		305			
	agggggataa ggagggaaca tatcataact gcactgtgat gaagaagctg ttccccacag				1080
	aggagaagct ctgctttctt tctctccaac ttctcctttt taaaatcagc atgatgtgcc				1140
	tgtgagcatg gaagagtcct ctcagaagaa tgttggccat gagactatca ttcagaggag				1200
	gaggggattt ctctcttcaa ggcataaaca gtggaagaac agtcatatgc cattggaagt				1260
15	cttgccagc agtcctgaat ccttcctgaa gagttcagaa aatagatgtg gtattgctct				1320
	gaggaccagg caggaggaac totacaacct gagtttgcc ttgtgaggca ttagtataga				1380
	ccaaataaaa agctgcagaa attggaaagt ttatgtttta aataaatgac tgtgat				1436
	<210> 82				
20	<211> 997				
	<212> DNA				
	<213> Homo sapiens				
	<220>				
	<221> CDS				
25	<222> (87)...(638)				
	<400> 82				
	gagacaaagc ggagaacgct ggtgggacctg ttgtggagta cgctttggac tgagaagcat				60
	cgaggctata ggacgcagct gttgcc atg acg gcc cag ggg ggc ctg gtg				110
30	Met Thr Ala Gln Gly Gly Leu Val				
		1	5		
	gct aac cga ggc cgg cgc ttc aag tgg gcc att gag cta agc ggg cct				158
	Ala Asn Arg Gly Arg Arg Phe Lys Trp Ala Ile Glu Leu Ser Gly Pro				
		10	15	20	
35	gga gga ggc agc agg ggt cga agt gac cgg ggc agt ggc cag gga gac				206

83/177

	Gly Gly Gly Ser Arg Gly Arg Ser Asp Arg Gly Ser Gly Gln Gly Asp	
	25 30 35 40	
	tog ctc tac cca gtc ggt tac ttg gac aag caa gtg cct gat acc agc	254
5	Ser Leu Tyr Pro Val Gly Tyr Leu Asp Lys Gln Val Pro Asp Thr Ser	
	45 50 55	
	gtg caa gag aca gac cgg atc ctg gtg gag aag cgc tgc tgg gac atc	302
	Val Gln Glu Thr Asp Arg Ile Leu Val Glu Lys Arg Cys Trp Asp Ile	
	60 65 70	
10	gcc ttg ggt ccc ctc aaa cag att ccc atg aat ctc ttc atc atg tac	350
	Ala Leu Gly Pro Leu Lys Gln Ile Pro Met Asn Leu Phe Ile Met Tyr	
	75 80 85	
	atg gca ggc aat act atc tcc atc ttc cct act atg atg gtg tgt atg	398
	Met Ala Gly Asn Thr Ile Ser Ile Phe Pro Thr Met Met Val Cys Met	
	90 95 100	
15	atg gcc tgg cga ccc att cag gca ctt atg gcc att tca gcc act ttc	446
	Met Ala Trp Arg Pro Ile Gln Ala Leu Met Ala Ile Ser Ala Thr Phe	
	105 110 115 120	
	aag atg tta gaa agt tca agc cag aag ttt ctt cag ggt ttg gtc tat	494
	Lys Met Leu Glu Ser Ser Ser Gln Lys Phe Leu Gln Gly Leu Val Tyr	
20	125 130 135	
	ctc att ggg aac ctg atg ggt ttg gca ttg gct gtt tac aag tgc cag	542
	Leu Ile Gly Asn Leu Met Gly Leu Ala Leu Ala Val Tyr Lys Cys Gln	
	140 145 150	
25	tcc atg gga ctg tta cct aca cat gca tcg gat tgg tta gcc ttc att	590
	Ser Met Gly Leu Leu Pro Thr His Ala Ser Asp Trp Leu Ala Phe Ile	
	155 160 165	
	gag ccc cct gag aga atg gag ttc agt ggt gga gga ctg ctt ttg tgaac	640
	Glu Pro Pro Glu Arg Met Glu Phe Ser Gly Gly Gly Leu Leu Leu	
	170 175 180	
30	atgagaaagc agcgccctggt ccctatgtat ttgggtctta ttacatcct tctttaagcc	700
	cagtggctcc tcagcataact cttaaactaa tcacttatgt taaaaagaac caaaagactc	760
	ttttctccat ggtggggtga caggtcctag aaggacaatg tgcattattac gacaaacaca	820
	aagaaactat accataacc aaggctgaaa ataatgtaga aaactttatt tttgtttcca	880
	gtacagagca aaacaacaac aaaaaaacat aactatgtaa acaagagaat aactgctgct	940
35	aatcaagaa ctgtttcagc atctccttcc aataaattaa atggttgaga acaatgc	997

84/177

<210> 83
 <211> 1753
 <212> DNA
 5 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (134)...(1117)

10 <400> 83
 tcttcagcgt cctaccgcgg gcactggctg cgagcgccgg gccacctgcg agtgtgcgca 60
 gggactctgg acaccgcgg cggcgagctg agggagcagt ctccacgagg acccaggcgg 120
 accctctggc gcc atg cgc gcc ctc ccc ggc ctg ctg gag gcc agg ggc 169
 Met Arg Ala Leu Pro Gly Leu Leu Glu Ala Arg Ala
 15 1 5 10
 cgt acg ccc cgg ctg ctc ctc ctc cag tgc ctt ctc gct gcc gcg cgc 217
 Arg Thr Pro Arg Leu Leu Leu Leu Gln Cys Leu Leu Ala Ala Ala Arg
 15 20 25
 cca agc tcg gcg gac ggc agt gcc cca gat tcg cct ttt aca agt cca 265
 20 Pro Ser Ser Ala Asp Gly Ser Ala Pro Asp Ser Pro Phe Thr Ser Pro
 30 35 40
 cct ctc aga gaa gaa ata atg gca aat aac ttt tcc ttg gag agt cat 313
 Pro Leu Arg Glu Glu Ile Met Ala Asn Asn Phe Ser Leu Glu Ser His
 45 50 55 60
 25 aac ata tca ctg act gaa cat tct agt atg cca gta gaa aaa aat atc 361
 Asn Ile Ser Leu Thr Glu His Ser Ser Met Pro Val Glu Lys Asn Ile
 65 70 75
 act tta gaa agg cct tct aat gta aat ctc aca tgc cag ttc aca aca 409
 Thr Leu Glu Arg Pro Ser Asn Val Asn Leu Thr Cys Gln Phe Thr Thr
 30 80 85 90
 tct ggg gat ttg aat gca gta aat gtg act tgg aaa aaa gat ggt gaa 457
 Ser Gly Asp Leu Asn Ala Val Asn Val Thr Trp Lys Lys Asp Gly Glu
 95 100 105
 caa ctt gag aat aat tat ctt gtc agt gca aca gga agc acc ttg tat 505
 35 Gln Leu Glu Asn Asn Tyr Leu Val Ser Ala Thr Gly Ser Thr Leu Tyr

85/177

	110	115	120	
	acc caa tac agg ttc acc atc att aat agc aaa caa atg gga agt tat	553		
	Thr Gln Tyr Arg Phe Thr Ile Ile Asn Ser Lys Gln Met Gly Ser Tyr			
	125	130	135	140
5	tct tgt ttc ttt cga gag gaa aag gaa caa agg gga aca ttt aat ttc	601		
	Ser Cys Phe Phe Arg Glu Glu Lys Glu Gln Arg Gly Thr Phe Asn Phe			
	145	150	155	
	aaa gtc cct gaa ctt cat ggg aaa aac aag cca ttg atc tct tac gta	649		
	Lys Val Pro Glu Leu His Gly Lys Asn Lys Pro Leu Ile Ser Tyr Val			
10	160	165	170	
	ggg gat tct act gtc ttg aca tgt aaa tgt caa aat tgt ttt cct tta	697		
	Gly Asp Ser Thr Val Leu Thr Cys Lys Cys Gln Asn Cys Phe Pro Leu			
	175	180	185	
	aat tgg acc tgg tac agt agt aat ggg agt gta aag gtt cct gtt ggt	745		
15	Asn Trp Thr Trp Tyr Ser Ser Asn Gly Ser Val Lys Val Pro Val Gly			
	190	195	200	
	gtt caa atg aat aaa tat gtg atc aat gga aca tat gct aac gaa aca	793		
	Val Gln Met Asn Lys Tyr Val Ile Asn Gly Thr Tyr Ala Asn Glu Thr			
	205	210	215	220
20	aag ctg aag ata aca caa ctt ttg gag gaa gat ggg gaa tct tac tgg	841		
	Lys Leu Lys Ile Thr Gln Leu Leu Glu Glu Asp Gly Glu Ser Tyr Trp			
	225	230	235	
	tgc cgt gca cta ttc caa tta ggc gag agt gaa gaa cac att gag ctt	889		
	Cys Arg Ala Leu Phe Gln Leu Gly Glu Ser Glu Glu His Ile Glu Leu			
25	240	245	250	
	gtg gtg ctg agc tat ttg gtg ccc ctc aaa cca ttt ctt gta ata gtg	937		
	Val Val Leu Ser Tyr Leu Val Pro Leu Lys Pro Phe Leu Val Ile Val			
	255	260	265	
	gct gag gtg att ctt tta gtg gcc acc att ctg ctt tgt gaa aag tac	985		
30	Ala Glu Val Ile Leu Leu Val Ala Thr Ile Leu Leu Cys Glu Lys Tyr			
	270	275	280	
	aca caa aag aaa aag aag cac tca gat gag ggg aaa gaa ttt gag cag	1033		
	Thr Gln Lys Lys Lys Lys His Ser Asp Glu Gly Lys Glu Phe Glu Gln			
	285	290	295	300
35	att gaa cag ctg aaa tca gat gat agc aat ggt ata gaa aat aat gtc	1081		

86/177

Ile Glu Gln Leu Lys Ser Asp Asp Ser Asn Gly Ile Glu Asn Asn Val
 305 310 315
 ccc agg cat aga aaa aat gag tct ctg ggc cag tgaatacaaa acatca 1130
 Pro Arg His Arg Lys Asn Glu Ser Leu Gly Gln
 5 320 325
 tgctcgagaat cattggaaga tatacagagt tcgtatttca gctttattta tccttcctgt 1190
 taagagcctc tgagttttta gttttaaaag gatgaaaagc ttatgcaaca tgctcagcag 1250
 gagcttcac c aacgatatat gtcagatcta aaggtatatt ttcattctgt aattatgtta 1310
 cataaaagca atgtaaatca gaataaatat gttagaccag aataaaatta attatattct 1370
 10 ggtcttcaaa ggacacacag aacagatata agcagaatca ctttaatactt catagaacaa 1430
 aaatcactca aaacctgttt ataaccaaag aattcatgaa aaagaaagcc tttgccattt 1490
 gtcttagaaa gttatttttt taaaaaaaat catacttact attagtattct atggaagtat 1550
 atgtaacaat ttttatgtaa aggtcatctt tctgtgatag tgaaaaaata tgtctttact 1610
 aagttgaaat gaatactttc tgccttttgc catgatagtt attctacaat ctccacaaga 1670
 15 aaaatatacc ttttatccgg aaatattggt ttaaggcaaa taaataaaac tgtgcttgc 1730
 ctaaagctct gcactacaaa agc 1753

<210> 84
 <211> 1117
 20 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (62)...(733)

25 <400> 84
 cgccccactt gtgtttcttc tcctgggtgca gagttgcaag caagtttata ggagtatcgc 60
 c atg aag ttc gtc ccc tgc ctc ctg ctg gtg acc ttg tcc tgc ctg 106
 Met Lys Phe Val Pro Cys Leu Leu Leu Val Thr Leu Ser Cys Leu
 30 1 5 10 15
 ggg act ttg ggt cag gcc ccg agg caa aag caa gga agc act ggg gag 154
 Gly Thr Leu Gly Gln Ala Pro Arg Gln Lys Gln Gly Ser Thr Gly Glu
 20 25 30
 gaa ttc cat ttc cag act gga ggg aga gat tcc tgc act atg cgt ccc 202
 35 Glu Phe His Phe Gln Thr Gly Gly Arg Asp Ser Cys Thr Met Arg Pro

87/177

	35	40	45	
	agc agc ttg ggg caa ggt gct gga gaa gtc tgg ctt cgc gtc gac tgc	250		
	Ser Ser Leu Gly Gln Gly Ala Gly Glu Val Trp Leu Arg Val Asp Cys			
	50	55	60	
5	cgc aac aca gac cag acc tac tgg tgt gag tac agg ggg cag ccc agc	298		
	Arg Asn Thr Asp Gln Thr Tyr Trp Cys Glu Tyr Arg Gly Gln Pro Ser			
	65	70	75	
	atg tgc cag gct ttc gct gct gac ccc aaa tct tac tgg aat caa gcc	346		
	Met Cys Gln Ala Phe Ala Ala Asp Pro Lys Ser Tyr Trp Asn Gln Ala			
10	80	85	90	95
	ctg cag gag ctg agg cgc ctt cac cat gcg tgc cag ggg gcc ccg gtg	394		
	Leu Gln Glu Leu Arg Arg Leu His His Ala Cys Gln Gly Ala Pro Val			
	100	105	110	
	ctt agg cca tcc gtg tgc agg gag gct gga ccc cag gcc cat atg cag	442		
15	Leu Arg Pro Ser Val Cys Arg Glu Ala Gly Pro Gln Ala His Met Gln			
	115	120	125	
	cag gtg act tcc agc ctc aag ggc agc cca gag ccc aac cag cag cct	490		
	Gln Val Thr Ser Ser Leu Lys Gly Ser Pro Glu Pro Asn Gln Gln Pro			
	130	135	140	
20	gag gct ggg acg cca tct ctg agg ccc aag gcc aca gtg aaa ctc aca	538		
	Glu Ala Gly Thr Pro Ser Leu Arg Pro Lys Ala Thr Val Lys Leu Thr			
	145	150	155	
	gaa gca aca cag ctg gga aag gac tcg atg gaa gag ctg gga aaa gcc	586		
	Glu Ala Thr Gln Leu Gly Lys Asp Ser Met Glu Glu Leu Gly Lys Ala			
25	160	165	170	175
	aaa ccc acc acc cga ccc aca gcc aaa cct acc cag cct gga ccc agg	634		
	Lys Pro Thr Thr Arg Pro Thr Ala Lys Pro Thr Gln Pro Gly Pro Arg			
	180	185	190	
	ccc gga ggg aat gag gaa gca aag aag aag gcc tgg gaa cat tgt tgg	682		
30	Pro Gly Gly Asn Glu Glu Ala Lys Lys Lys Ala Trp Glu His Cys Trp			
	195	200	205	
	aaa ccc ttc cag gcc ctg tgc gcc ttt ctc atc agc ttc ttc cga ggg	730		
	Lys Pro Phe Gln Ala Leu Cys Ala Phe Leu Ile Ser Phe Phe Arg Gly			
	210	215	220	
35	tgacaggtga aagaccccta cagatctgac ctctccctga cagacaacca tctcttttta	790		

88/177

	tattatgccg ctttcaatcc aacgttctca cactggaaga agagagtttc taatcagatg	850
	caacggccca aattcttgat ctgcagcttc tctgaagttt ggaaaagaaa ccttcctttc	910
	tggagtttgc agagttcagc aatatgatag ggaacaggtg ctgatgggcc caagagtgc	970
	aagcatacac aactacttat tatctgtaga agttttgctt tgttgatctg agccttctat	1030
5	gaaagtttaa atatgtaacg cattcatgaa tttccagtgt tcagtaaata gcagctatgt	1090
	gtgtgcaaaa taaaagaatg atttcag	1117
	<210> 85	
	<211> 1380	
10	<212> DNA	
	<213> Homo sapiens	
	<220>	
	<221> CDS	
	<222> (43)...(189)	
15	<400> 85	
	gcagtctgtc tgagggcggc cgaagtggct ggctcattta ag atg agg ctt ctg	54
	Met Arg Leu Leu	
	1	
20	ctg ctt ctc cta gtg gcg gcg tct gcg atg gtc cgg agc gag gcc tcg	102
	Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg Ser Glu Ala Ser	
	5 10 15 20	
	gcc aat ctg gcc gcc gtg ccc agc aag aga tta aag atg cag tac gcc	150
	Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys Met Gln Tyr Ala	
25	25 30 35	
	acg ggg ccg ctg ctc aag ttc cag att tgt gtt tcc tgag	190
	Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser	
	40 45	
	gttataggcg ggtgtttgag gagtacatgc gggttattag ccagcggtag ccagacatcc	250
30	gcattgaagg agagaattac ctccctcaac caatatatag acacatagca tctttcctgt	310
	cagtcttcaa actagtatta ataggcttaa taattgttgg caaggatcct tttgctttct	370
	ttggcatgca agctcctagc atctggcagt ggggccaaga aaataagggtt tatgcattgta	430
	tgatggtttt cttcttgagc aacatgattg agaaccagtg tatgtcaaca ggtgcatttg	490
	agataacttt aaatgatgta cctgtgtggt ctaagctgga atctggtcac cttccatcca	550
35	tgcaacaact tgttcaaatt cttgacaatg aaatgaagct caatgtgcat atggattcaa	610

89/177

	tcccacacca tcgatcatag caccacotat cagcactgaa aactcttttg cattaagggga	670
	tcattgcaag agcagcgtga ctgacattat gaaggcctgt actgaagaca gcaagctgtt	730
	agtacagacc agatgctttc ttggcagget cgttgtacct cttggaaaac ctcaatgcaa	790
	gatagtgttt cagtgtctggc atattttgga attctgcaca ttcattggagt gcaataatac	850
5	tgtatagctt tcccacctc ccacaaaatc acccagttaa tgtgtgtgtg tgtttttttt	910
	tttaaggtaa acattactac ttgtaacttt ttttcttagt catatttgaa aaagtagaaa	970
	attgagttac aatttgattt tttttccaaa gatgtctgtt aaatctgttg tgcttttata	1030
	tgaatatttg ttttttatag tttaaaattg atcctttggg aatccagttg aagttcccaa	1090
	atactttata agagttttatc agacatctct aatttggcca tgtccagttt atacagttta	1150
10	caaaatatag cagatgcaag attatggggg aaatcctata ttcagagtac tctataaatt	1210
	tttgtgtatg tgtgtatgtg cgtgtgatta ccagagaact actaaaaaaaa ccaactgctt	1270
	tttaaatact attgtgtagt taaagtgtca tgccttgacc aatctaataga attgattaat	1330
	taactggggc tttatactta actaaataaa aaactaagca gatatgagtt	1380
15	<210> 86	
	<211> 1503	
	<212> DNA	
	<213> Homo sapiens	
	<220>	
20	<221> CDS	
	<222> (51)...(1166)	
	<400> 86	
25	gtgacggggc cgggcgccgc taactggagc gaaccccagc gtccgccgac atg gcc	56
	Met Ala	
	1	
	tgg acc aag tac cag ctg ttc ctg gcc ggg ctc atg ctt gtt acc ggc	104
	Trp Thr Lys Tyr Gln Leu Phe Leu Ala Gly Leu Met Leu Val Thr Gly	
	5 10 15	
30	tcc atc aac acg ctc tcg gca aaa tgg gcg gac aat ttc atg gcc gag	152
	Ser Ile Asn Thr Leu Ser Ala Lys Trp Ala Asp Asn Phe Met Ala Glu	
	20 25 30	
	ggc tgt gga ggg agc aag gag cac agc ttc cag cat ccc ttc ctc cag	200
	Gly Cys Gly Gly Ser Lys Glu His Ser Phe Gln His Pro Phe Leu Gln	
35	35 40 45 50	

90/177

	gca gtg ggc atg ttc ctg gga gaa ttc tcc tgc ctg gct gcc ttc tac	248
	Ala Val Gly Met Phe Leu Gly Glu Phe Ser Cys Leu Ala Ala Phe Tyr	
	55 60 65	
	ctc ctc cga tgc aga gct gca ggg caa tca gac tcc agc gta gac ccc	296
5	Leu Leu Arg Cys Arg Ala Ala Gly Gln Ser Asp Ser Ser Val Asp Pro	
	70 75 80	
	cag cag ccc ttc aac cct ctt ctt ttc ctg ccc cca gcg ctc tgt gac	344
	Gln Gln Pro Phe Asn Pro Leu Leu Phe Leu Pro Pro Ala Leu Cys Asp	
	85 90 95	
10	atg aca ggg acc agc ctc atg tat gtg gct ctg aac atg acc agt gcc	392
	Met Thr Gly Thr Ser Leu Met Tyr Val Ala Leu Asn Met Thr Ser Ala	
	100 105 110	
	tcc agc ttc cag atg ctg cgg ggt gca gtg atc ata ttc act ggc ctg	440
	Ser Ser Phe Gln Met Leu Arg Gly Ala Val Ile Ile Phe Thr Gly Leu	
15	115 120 125 130	
	ttc tcg gtg gcc ttc ctg ggc cgg agg ctg gtg ctg agc cag tgg ctg	488
	Phe Ser Val Ala Phe Leu Gly Arg Arg Leu Val Leu Ser Gln Trp Leu	
	135 140 145	
	ggc atc cta gcc acc atc gcg ggg ctg gtg gtc gtg ggc ctg gct gac	536
20	Gly Ile Leu Ala Thr Ile Ala Gly Leu Val Val Val Gly Leu Ala Asp	
	150 155 160	
	ctc ctg agc aag cac gac agt cag cac aag ctc agc gaa gtg atc aca	584
	Leu Leu Ser Lys His Asp Ser Gln His Lys Leu Ser Glu Val Ile Thr	
	165 170 175	
25	ggg gac ctg ttg atc atc atg gcc cag atc atc gtt gcc atc cag atg	632
	Gly Asp Leu Leu Ile Ile Met Ala Gln Ile Ile Val Ala Ile Gln Met	
	180 185 190	
	gtg cta gag gag aag ttc gtc tac aaa cac aat gtg cac cca ctg cgg	680
	Val Leu Glu Glu Lys Phe Val Tyr Lys His Asn Val His Pro Leu Arg	
30	195 200 205 210	
	gca gtt ggc act gag ggc ctc ttt ggc ttt gtg atc ctc tcc ctg ctg	728
	Ala Val Gly Thr Glu Gly Leu Phe Gly Phe Val Ile Leu Ser Leu Leu	
	215 220 225	
	ctg gtg ccc atg tac tac atc ccc gcc ggc tcc ttc agc gga aac cct	776
35	Leu Val Pro Met Tyr Tyr Ile Pro Ala Gly Ser Phe Ser Gly Asn Pro	

91/177

	230	235	240	
	cgt ggg aca ctg gag gat gca ttg gac gcc ttc tgc cag gtg ggc cag			824
	Arg Gly Thr Leu Glu Asp Ala Leu Asp Ala Phe Cys Gln Val Gly Gln			
	245	250	255	
5	cag ccg ctc att gcc gtg gca ctg ctg ggc aac atc agc agc att gcc			872
	Gln Pro Leu Ile Ala Val Ala Leu Leu Gly Asn Ile Ser Ser Ile Ala			
	260	265	270	
	ttc ttc aac ttc gca ggc atc agc gtc acc aag gaa ctg agc gcc acc			920
	Phe Phe Asn Phe Ala Gly Ile Ser Val Thr Lys Glu Leu Ser Ala Thr			
10	275	280	285	290
	acc cgc atg gtg ttg gac agc ttg cgc acc gtt gtc atc tgg gca ctg			968
	Thr Arg Met Val Leu Asp Ser Leu Arg Thr Val Val Ile Trp Ala Leu			
	295	300	305	
	agc ctg gca ctg ggc tgg gag gcc ttc cat gca ctg cag atc ctt ggc			1016
15	Ser Leu Ala Leu Gly Trp Glu Ala Phe His Ala Leu Gln Ile Leu Gly			
	310	315	320	
	ttc ctc ata ctc ctt ata ggc act gcc ctc tac aat ggg cta cac cgt			1064
	Phe Leu Ile Leu Leu Ile Gly Thr Ala Leu Tyr Asn Gly Leu His Arg			
	325	330	335	
20	ccg ctg ctg ggc cgc ctg tcc agg ggc cgg ccc ctg gca gag gag agc			1112
	Pro Leu Leu Gly Arg Leu Ser Arg Gly Arg Pro Leu Ala Glu Glu Ser			
	340	345	350	
	gag cag gag aga ctg ctg ggt ggc acc cgc act ccc atc aat gat gcc			1160
	Glu Gln Glu Arg Leu Leu Gly Gly Thr Arg Thr Pro Ile Asn Asp Ala			
25	355	360	365	370
	agc tgagggtccc tggaggcttc tactgccacc cgggtgctcc ttctccc			1210
	Ser			
	tgagactgag gccacacagg ctggtgggcc ccgaatgcc tatccccaag gcctcaccct			1270
30	gtcccccctccc tgcagaaccc ccagggcagc tgctgccaca gaagataaca acacccaagt			1330
	cctcttttttc tcactaccac ctgcagggtg gtgttaccca gccccacaa gcctgagtgc			1390
	agtggcagac ctcagctetc tggacccttc ctacagcact agagctaaat catgaagttg			1450
	aattgtagga atttaccacc gtagtgtatc tgaatcataa actagattat cat			1503
35	<210> 87			

92/177

<211> 733

<212> DNA

<213> Homo sapiens

<220>

5 <221> CDS

<222> (40)...(312)

<400> 87

```

gttaaggcac acagagcacc agctccctcc tgccctgaag atg ttc cac caa att      54
10                                     Met Phe His Gln Ile
                                     1           5
tgg gca gct ctg ctc tac ttc tat ggt att atc ctt aac tcc atc tac      102
Trp Ala Ala Leu Leu Tyr Phe Tyr Gly Ile Ile Leu Asn Ser Ile Tyr
                                     10           15           20
15 cag tgc cct gag cac agt caa ctg aca act ctg ggc gtg gat ggg aag      150
Gln Cys Pro Glu His Ser Gln Leu Thr Thr Leu Gly Val Asp Gly Lys
                                     25           30           35
gag ttc cca gag gtc cac ttg ggc cag tgg tac ttt atc gca ggg gca      198
Glu Phe Pro Glu Val His Leu Gly Gln Trp Tyr Phe Ile Ala Gly Ala
20                                     40           45           50
gct ccc acc aag gag gag ttg gca act ttt gac cct gtg gac aac att      246
Ala Pro Thr Lys Glu Glu Leu Ala Thr Phe Asp Pro Val Asp Asn Ile
                                     55           60           65
gtc ttc aat atg gct gct ggc tct gcc ccg atg cag ctc cac ctt cgt      294
25 Val Phe Asn Met Ala Ala Gly Ser Ala Pro Met Gln Leu His Leu Arg
                                     70           75           80           85
gct acc atc cgc atg tgagtggaaa gatgggctct gtgtgccccg g      340
Ala Thr Ile Arg Met
                                     90
30 aaatggatct accacctgac tgaagggagc acagatctca gaactgaagg ccgccctgac      400
atgaagactg agctcttttc cagctcatgc ccaggtggaa tcatgctgaa tgagacaggc      460
caggggttacc agcgcctttct cctctacaat cgctcaccac atcctcccga aaagtgtgtg      520
gaggaattca agtccctgac ttccctgctg gactccaaag ccttcttatt gactcctagg      580
aatcaagagg cctgtgagct gtccaataac tgacctgtaa cttcatctaa gtccccagat      640
35 ggggtacaatg ggagctgagt tgttgaggag agaagctgga gacttccagc tccagctccc      700

```

93/177

actcaagata ataaagataa tttttcaatc etc

733

<210> 88

<211> 3768

5 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (358)...(1857)

10

<400> 88

gctagtggcg cgcgaggag cgacgcgtgg agaagcggcc cacgtgtctg ccagagtgca 60

agtcctgtgt tcttcccgct ccttacgcat ccgcgggtcca gggcgccctt tcagccccgc 120

tggtgttcgc ccaccccggg ccgcgtgagt ggggccccac gcagctcccc gcaactcgtg 180

15 ggccaacttg gccaaagcaac tctgtccggg ggcgggtgct tgcggggggg gagtaccggg 240

cactgcgcat gcggagctcc aaattcaaac agctgttttc agaggctgga gggcgggcgg 300

actggtagca gctgggggcta ggagaggctt tctctaggag gcggcgcgtc gggagcc 357

20 atg gtg gac cgg ggc cct ctg ctc acc tcg gcc atc atc ttc tac ctg 405

Met Val Asp Arg Gly Pro Leu Leu Thr Ser Ala Ile Ile Phe Tyr Leu

1 5 10 15

gcc atc ggg gcg gcg atc ttc gaa gtg ctg gag gag cca cac tgg aag 453

Ala Ile Gly Ala Ala Ile Phe Glu Val Leu Glu Glu Pro His Trp Lys

25 20 25 30

gag gcc aag aaa aac tactac aca cag aag ctg cat ctg ctc aag gag 501

Glu Ala Lys Lys Asn Tyr Tyr Thr Gln Lys Leu His Leu Leu Lys Glu

35 40 45

ttc ccg tgc ctg ggt cag gag ggc ctg gac aag atc cta gag gtg gta 549

30 Phe Pro Cys Leu Gly Gln Glu Gly Leu Asp Lys Ile Leu Glu Val Val

50 55 60

tct gat gct gca gga cag ggt gtg gcc atc aca ggg aac cag acc ttc 597

Ser Asp Ala Ala Gly Gln Gly Val Ala Ile Thr Gly Asn Gln Thr Phe

65 70 75 80

35 aac aac tgg aac tgg ccc aat gca atg att ttt gca gcg acc gtc att 645

94/177

	Asn Asn Trp Asn Trp Pro Asn Ala Met Ile Phe Ala Ala Thr Val Ile	
	85 90 95	
	acc acc att gga tat ggc aat gtg gct ccc aag acc ccc gcc ggt cgc	693
	Thr Thr Ile Gly Tyr Gly Asn Val Ala Pro Lys Thr Pro Ala Gly Arg	
5	100 105 110	
	ctc ttc tgt gtt ttc tat ggt ctc ttc ggg gtg ccg ctc tgc ctg acg	741
	Leu Phe Cys Val Phe Tyr Gly Leu Phe Gly Val Pro Leu Cys Leu Thr	
	115 120 125	
	tgg atc agt gcc ctg ggc aag ttc ttc ggg gga cgt gcc aag aga cta	789
10	Trp Ile Ser Ala Leu Gly Lys Phe Phe Gly Gly Arg Ala Lys Arg Leu	
	130 135 140	
	ggg cag ttc ctt acc aag aga ggt gtg agt ctg cgg aag gcg cag atc	837
	Gly Gln Phe Leu Thr Lys Arg Gly Val Ser Leu Arg Lys Ala Gln Ile	
	145 150 155 160	
15	acg tgc aca gtc atc ttc atc gtg tgg ggc gtc cta gtc cac ctg gtg	885
	Thr Cys Thr Val Ile Phe Ile Val Trp Gly Val Leu Val His Leu Val	
	165 170 175	
	atc cca ccc ttc gta ttc atg gtg act gag ggg tgg aac tac atc gag	933
	Ile Pro Pro Phe Val Phe Met Val Thr Glu Gly Trp Asn Tyr Ile Glu	
20	180 185 190	
	ggc ctc tac tac tcc ttc atc acc atc tcc acc atc ggc ttc ggt gac	981
	Gly Leu Tyr Tyr Ser Phe Ile Thr Ile Ser Thr Ile Gly Phe Gly Asp	
	195 200 205	
	ttt gtg gcc ggt gtg aac ccc agc gcc aac tac cac gcc ctg tac cgc	1029
25	Phe Val Ala Gly Val Asn Pro Ser Ala Asn Tyr His Ala Leu Tyr Arg	
	210 215 220	
	tac ttc gtg gag ctc tgg atc tac ttg ggg ctg gcc tgg ctg tcc ctt	1077
	Tyr Phe Val Glu Leu Trp Ile Tyr Leu Gly Leu Ala Trp Leu Ser Leu	
	225 230 235 240	
30	ttt gtc aac tgg aag gtg agc atg ttt gtg gaa gtc cac aaa gcc att	1125
	Phe Val Asn Trp Lys Val Ser Met Phe Val Glu Val His Lys Ala Ile	
	245 250 255	
	aag aag cgg cgg cgg cga cgg aag gag tcc ttt gag agc tcc cca cac	1173
	Lys Lys Arg Arg Arg Arg Arg Lys Glu Ser Phe Glu Ser Ser Pro His	
35	260 265 270	

95/177

	tcc cgg aag gcc ctg cag gtg aag ggg agc aca gcc tcc aag gac gtc	1221
	Ser Arg Lys Ala Leu Gln Val Lys Gly Ser Thr Ala Ser Lys Asp Val	
	275 280 285	
	aac atc ttc agc ttt ctt tcc aag aag gaa gag acc tac aac gac ctc	1269
5	Asn Ile Phe Ser Phe Leu Ser Lys Lys Glu Glu Thr Tyr Asn Asp Leu	
	290 295 300	
	atc aag cag atc ggg aag aag gcc atg aag aca agc ggg ggt ggg gag	1317
	Ile Lys Gln Ile Gly Lys Lys Ala Met Lys Thr Ser Gly Gly Gly Glu	
	305 310 315 320	
10	acg ggc ccg ggc cca ggg ctg ggg cct caa ggc ggt ggg ctc cca gca	1365
	Thr Gly Pro Gly Pro Gly Leu Gly Pro Gln Gly Gly Gly Leu Pro Ala	
	325 330 335	
	ctg ccc cct tcc ctg gtg ccc ctg gta gtc tac tcc aag aac egg gtg	1413
	Leu Pro Pro Ser Leu Val Pro Leu Val Val Tyr Ser Lys Asn Arg Val	
15	340 345 350	
	ccc acc ttg gaa gag gtg tca cag aca ctg agg agc aaa ggc cac gta	1461
	Pro Thr Leu Glu Glu Val Ser Gln Thr Leu Arg Ser Lys Gly His Val	
	355 360 365	
	tca agg tcc cca gat gag gag gct gtg gca cgg gcc cct gaa gac agc	1509
20	Ser Arg Ser Pro Asp Glu Glu Ala Val Ala Arg Ala Pro Glu Asp Ser	
	370 375 380	
	tcc cct gcc ccc gag gtg ttc atg aac cag ctg gac cgc atc agc gag	1557
	Ser Pro Ala Pro Glu Val Phe Met Asn Gln Leu Asp Arg Ile Ser Glu	
	385 390 395 400	
25	gaa tgc gag cca tgg gac gcc cag gac tac cac cca ctc atc ttc cag	1605
	Glu Cys Glu Pro Trp Asp Ala Gln Asp Tyr His Pro Leu Ile Phe Gln	
	405 410 415	
	gac gcc agc atc acc ttc gtg aac acg gag gct ggc ctc tca gac gag	1653
	Asp Ala Ser Ile Thr Phe Val Asn Thr Glu Ala Gly Leu Ser Asp Glu	
30	420 425 430	
	gag acc tcc aag tcc tcg cta gag gac aac ttg gca ggg gag gag agc	1701
	Glu Thr Ser Lys Ser Ser Leu Glu Asp Asn Leu Ala Gly Glu Glu Ser	
	435 440 445	
	ccc cag cag ggg gct gaa gcc aag gcg ccc ctg aac atg ggc gag ttc	1749
35	Pro Gln Gln Gly Ala Glu Ala Lys Ala Pro Leu Asn Met Gly Glu Phe	

96/177

	450	455	460	
	ccc tcc tcc tcc gag tcc acc ttc acc agc act gag tct gag ctc tct			1797
	Pro Ser Ser Ser Glu Ser Thr Phe Thr Ser Thr Glu Ser Glu Leu Ser			
	465	470	475	480
5	gtg cct tac gaa cag ctg atg aat gag tac aac aag gct aac agc ccc			1845
	Val Pro Tyr Glu Gln Leu Met Asn Glu Tyr Asn Lys Ala Asn Ser Pro			
	485	490	495	
	aag ggc aca tgaggcaggg ccggctcccc accccacctt tgatgg			1890
	Lys Gly Thr			
10				
	cctcttcccc cctcacccta ggggtgtcccg agatgaccgg gacgcctggc ccttgggtggg			1950
	ggggcagcct cggaactggg agtggggggc caggggcctt cctaaccttc catcatcccc			2010
	agctagatgt atgcccggga cagggcctct gttctccagc tgaaccatac cctggctgtg			2070
	ggggcatctg tcttgagctt ggctgggtgta tctcacaatg caaagacatg ctggctggcg			2130
15	ggacaggtgg gcaggactga ccctgaggag gccttgcttg caggggtcttt gtcccaccat			2190
	ttgggtggagt atcacacggg tctctgaggt ccgggggcctc agctgtttta gtttaccggt			2250
	attactgagc tcggcatttg gagagggagc tctgaagtgt ctggggaggt accgctgtgc			2310
	gtgggggtcag gtgtttccgt accacagcag gagcaggggc cgcccgcata ccagctgtgg			2370
	gcctgccggg caggtcgggc acctactaca aaccgtagtg ggggtggaggc tgctggaggt			2430
20	gggagtgagg agatgagggc aggggtctcaa acagtcctga ctcacagggc ctggaaacaa			2490
	gtcctatgtg ggccctggggc ctgggggtcct cactctcctt gttgggtctac tcaggcccag			2550
	cccagagctg tgttccctgt ctcaggtcaa gcagtggcag acgcaaggct ttctgtgggc			2610
	ccccaagtgg taggagggag agtagcagag catgggttac tgggaagccgg gactgctagg			2670
	gtggtgtggc agggagctgc aagagtgagg ctcagctctg gctgggtctg cccttaccac			2730
25	tcctgcccgc cggagaactg cacaccctgc ccgctggccc caggacctgc actcccaatc			2790
	ctgctgtctt ctccttccct gtgccctgaa caaggacctc actgcccgc tccccctccc			2850
	accagccccc ttggggccagg caggggtgagg ccaaattgct cttggcccac aaatgggtga			2910
	tggtcagata tgtgaatcaa gtcctttct ctagctagtg tttgatgtgc acgtgtgtgt			2970
	gcacagtgcg tgtgtgcaca cgcacacctg tgcactcgtg tgtgtttaag aaaggaaagg			3030
30	atttgggctg gggagcaaaa gataatgtga aactgttggt ggactctctg gtgaggggtg			3090
	ggcagaactt gctgctacta gagttcttgg gttctccatg atgttcaccc tggggctggc			3150
	ccactgtgtc ctgaatgttt ttgttatttt ttgttttatt ttttaacaa actgctgttt			3210
	ttatatacct ggaatctgtt gttggcttca gagccagtgg ttaaagagca ggggtcccaag			3270
	gattgggaga tctagtgtct gccctcctgc cctgcaactc aattgggcct ttttcggtga			3330
35	cctcatccaa ggccatgatg tcaagggcca tgtccccaag cagaggtgga gaaggggaca			3390

97/177

ctgaggtgag caaaagcagg aaggggcata cactgcgggt gactggagggc cgggcaggaa 3450
 gcaagtcata agagccgctc agctccgttc actctctgcc ttctgcecca ctactgtggg 3510
 gcagtggggc cagagcccac ctccccaaca tgtgaagaca gtgatgggca cgtgccca 3570
 ccccaacttc totagccgtt tgcagaggcc gccaccacagc aggggcctga aaaggagcag 3630
 5 cctcgatattt ttctgtgaaa tgttttaatg aaccatgttg ttgctggttg tcctggcacc 3690
 gcgcacactg tatgtacata ctggcaacga tgtcaaagt aattttattt aacattttta 3750
 caataaaaca tgaggtgg 3768

<210> 89
 10 <211> 770
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 15 <222> (24)...(344)

<400> 89
 accgcgaagg gaggagtggc aac atg gcg tct tcg gga gct ggt gac cct ctg 53
 Met Ala Ser Ser Gly Ala Gly Asp Pro Leu
 20 1 5 10
 gat tct aag cgt gga gag gcc ccg ttc gct cag cgt atc gac ccg act 101
 Asp Ser Lys Arg Gly Glu Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr
 15 20 25
 cgg gag aag ctg aca ccc gag caa ctg cat tcc atg cgg cag gcg gag 149
 25 Arg Glu Lys Leu Thr Pro Glu Gln Leu His Ser Met Arg Gln Ala Glu
 30 35 40
 ctt gcc cag tgg cag aag gtc cta cca cgg cgg cga acc cgg aac atc 197
 Leu Ala Gln Trp Gln Lys Val Leu Pro Arg Arg Arg Thr Arg Asn Ile
 45 50 55
 30 gtg acc ggc cta ggc atc ggg gcc ctg gtg ttg gct att tat ggt tac 245
 Val Thr Gly Leu Gly Ile Gly Ala Leu Val Leu Ala Ile Tyr Gly Tyr
 60 65 70
 acc ttc tac tcg att tcc cag gag cgt ttc cta gat gag cta gaa gac 293
 Thr Phe Tyr Ser Ile Ser Gln Glu Arg Phe Leu Asp Glu Leu Glu Asp
 35 75 80 85 90

98/177

	gag gcc aaa gct gcc cga gcc cga gct ctg gca agg gcg tca ggg tcc	341
	Glu Ala Lys Ala Ala Arg Ala Arg Ala Leu Ala Arg Ala Ser Gly Ser	
	95 100 105	
	taatctgga tgggtattga tcatgtccaa cctgctggag ccccttcaca tgggtggatga	400
5	tgccccatga ccctgtagaa attgaatect gctcacaaca ttgttggcct tottactaac	460
	cttggaccgt gattgagccc aagaaaccag ggacttacgc atttggccaa tgtcaaaaga	520
	acagaacttt gcccaactgca cacttgctgt gtacaatgac tgagcccttt cttgtagttt	580
	gtttccttgt ttgagaggtg tgcattgcgac cgtggctttt cccaaagttt ctgactttgt	640
	ggtttacccc ctteaccttc cagggacgca gttgttacga ggtagacgt ggcagctctg	700
10	tgcagtgttt gagcctacag tgggatacat aggggtcaaat tgagaataat aaactgagtc	760
	attctcctgg	770
	<210> 90	
	<211> 1229	
15	<212> DNA	
	<213> Homo sapiens	
	<220>	
	<221> CDS	
	<222> (96)...(554)	
20	<400> 90	
	cctactcctg gattaggagg actgacaata ctacatatat cattaagcat gggcctcgct	60
	tagaagttgc atctgagaaa gtageccaga agaca atg gac tat gtg tgc tgt	113
	Met Asp Tyr Val Cys Cys	
25	1 5	
	gct tac aac aac ata acc ggc agg caa gat gaa act cat ttc aca gtt	161
	Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu Thr His Phe Thr Val	
	10 15 20	
	atc atc act tcc gta gga ctg gag aag ctt gca cag aaa gga aaa tca	209
30	Ile Ile Thr Ser Val Gly Leu Glu Lys Leu Ala Gln Lys Gly Lys Ser	
	25 30 35	
	ttg tca cct tta gca agt ata act gga ata tca cta ttt ttg att ata	257
	Leu Ser Pro Leu Ala Ser Ile Thr Gly Ile Ser Leu Phe Leu Ile Ile	
	40 45 50	
35	tcc atg tgt ctt ctc ttc cta tgg aaa aaa tat caa ccc tac aaa gtt	305

99/177

Ser Met Cys Leu Leu Phe Leu Trp Lys Lys Tyr Gln Pro Tyr Lys Val
 55 60 65 70
 ata aaa cag aaa cta gaa ggc agg cca gaa aca gaa tac agg aaa gct 353
 Ile Lys Gln Lys Leu Glu Gly Arg Pro Glu Thr Glu Tyr Arg Lys Ala
 5 75 80 85
 caa aca ttt tca ggc cat gaa gat gct ctg gat gac ttc gga ata tat 401
 Gln Thr Phe Ser Gly His Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr
 90 95 100
 gaa ttt gtt gct ttt cca gat gtt tct ggt gtt tcc agg atc cca agc 449
 10 Glu Phe Val Ala Phe Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser
 105 110 115
 agg tct gtt cca gcc tct gat tgt gta tgc ggg caa gat ttg cac agt 497
 Arg Ser Val Pro Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser
 120 125 130
 15 aca gtg tat gaa gtt att cag cac atc cct gcc cag cag caa gac cat 545
 Thr Val Tyr Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His
 135 140 145 150
 cca gag tgaactttca tgggctaaac agtacattcg agtgaaattc tgaagaaac 600
 Pro Glu
 20
 attttaagga aaaacagtgg aaaagtatat taatctggaa tcagtgaaga aaccaagacc 660
 aacacctctt actcattatt cctttacatg cagaatagag gcatttatgc aaattgaact 720
 gcaggttttt cagcatatac acaatgtctt gtgcaacaga aaaacatggt ggggaaatat 780
 tctcagtggt agagtcgttc tcatgctgac ggggagaacg aaagtgcag gggtttcctc 840
 25 ataagttttg tatgaaatat ctctacaaac ctcaattagt tctactctac actttcacta 900
 tcatcaacac tgagactatc ctgtctcacc tacaaatgtg gaaactttac attgttcgat 960
 ttttcagcag actttgtttt attaaatttt tattagtgtt aagaatgcta aagtttcaat 1020
 tttatttcca aatttctatc ttgttatttg tacaacaaag taataaggat gggtgtcaca 1080
 aaaacaaaac tatgccttct cttttttttc aatcaccagt agtatttttg agaagacttg 1140
 30 tgaacactta aggaaatgac tattaaagtc ttatttttat ttttttcaag gaaagatgga 1200
 ttcaaataaa ttattctggt tttgctttt 1229

 <210> 91
 <211> 358
 35 <212> PRT

<213> Homo sapience

	Met	Ala	Pro	Gln	Asn	Leu	Ser	Thr	Phe	Cys	Leu	Leu	Leu	Leu	Tyr	Leu
5	1				5					10						15
	Ile	Gly	Ala	Val	Ile	Ala	Gly	Arg	Asp	Phe	Tyr	Lys	Ile	Leu	Gly	Val
				20					25					30		
	Pro	Arg	Ser	Ala	Ser	Ile	Lys	Asp	Ile	Lys	Lys	Ala	Tyr	Arg	Lys	Leu
			35					40					45			
10	Ala	Leu	Gln	Leu	His	Pro	Asp	Arg	Asn	Pro	Asp	Asp	Pro	Gln	Ala	Gln
		50					55					60				
	Glu	Lys	Phe	Gln	Asp	Leu	Gly	Ala	Ala	Tyr	Glu	Val	Leu	Ser	Asp	Ser
	65					70					75					80
	Glu	Lys	Arg	Lys	Gln	Tyr	Asp	Thr	Tyr	Gly	Glu	Glu	Gly	Leu	Lys	Asp
15					85					90						95
	Gly	His	Gln	Ser	Ser	His	Gly	Asp	Ile	Phe	Ser	His	Phe	Phe	Gly	Asp
				100					105					110		
	Phe	Gly	Phe	Met	Phe	Gly	Gly	Thr	Pro	Arg	Gln	Gln	Asp	Arg	Asn	Ile
		115						120					125			
20	Pro	Arg	Gly	Ser	Asp	Ile	Ile	Val	Asp	Leu	Glu	Val	Thr	Leu	Glu	Glu
		130					135					140				
	Val	Tyr	Ala	Gly	Asn	Phe	Val	Glu	Val	Val	Arg	Asn	Lys	Pro	Val	Ala
	145					150					155					160
	Arg	Gln	Ala	Pro	Gly	Lys	Arg	Lys	Cys	Asn	Cys	Arg	Gln	Glu	Met	Arg
25					165					170						175
	Thr	Thr	Gln	Leu	Gly	Pro	Gly	Arg	Phe	Gln	Met	Thr	Gln	Glu	Val	Val
				180					185					190		
	Cys	Asp	Glu	Cys	Pro	Asn	Val	Lys	Leu	Val	Asn	Glu	Glu	Arg	Thr	Leu
		195						200					205			
30	Glu	Val	Glu	Ile	Glu	Pro	Gly	Val	Arg	Asp	Gly	Met	Glu	Tyr	Pro	Phe
		210					215					220				
	Ile	Gly	Glu	Gly	Glu	Pro	His	Val	Asp	Gly	Glu	Pro	Gly	Asp	Leu	Arg
	225					230					235					240
	Phe	Arg	Ile	Lys	Val	Val	Lys	His	Pro	Ile	Phe	Glu	Arg	Arg	Gly	Asp
35					245					250						255

101/177

Asp Leu Tyr Thr Asn Val Thr Ile Ser Leu Val Glu Ser Leu Val Gly
 260 265 270
 Phe Glu Met Asp Ile Thr His Leu Asp Gly His Lys Val His Ile Ser
 275 280 285
 5 Arg Asp Lys Ile Thr Arg Pro Gly Ala Lys Leu Trp Lys Lys Gly Glu
 290 295 300
 Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile
 305 310 315 320
 Thr Phe Asp Val Asp Phe Pro Lys Glu Gln Leu Thr Glu Glu Ala Arg
 10 325 330 335
 Glu Gly Ile Lys Gln Leu Leu Lys Gln Gly Ser Val Gln Lys Val Tyr
 340 345 350
 Asn Gly Leu Gln Gly Tyr
 355
 15
 <210> 92
 <211> 226
 <212> PRT
 <213> Homo sapience
 20
 <400> 92
 Met Lys Met Val Ala Pro Trp Thr Arg Phe Tyr Ser Asn Ser Cys Cys
 1 5 10 15
 Leu Cys Cys His Val Arg Thr Gly Thr Ile Leu Leu Gly Val Trp Tyr
 25 20 25 30
 Leu Ile Ile Asn Ala Val Val Leu Leu Ile Leu Leu Ser Ala Leu Ala
 35 40 45
 Asp Pro Asp Gln Tyr Asn Phe Ser Ser Ser Glu Leu Gly Gly Asp Phe
 50 55 60
 30 Glu Phe Met Asp Asp Ala Asn Met Cys Ile Ala Ile Ala Ile Ser Leu
 65 70 75 80
 Leu Met Ile Leu Ile Cys Ala Met Ala Thr Tyr Gly Ala Tyr Lys Gln
 85 90 95
 Arg Ala Ala Trp Ile Ile Pro Phe Phe Cys Tyr Gln Ile Phe Asp Phe
 35 100 105 110

102/177

Ala Leu Asn Met Leu Val Ala Ile Thr Val Leu Ile Tyr Pro Asn Ser
115 120 125
Ile Gln Glu Tyr Ile Arg Gln Leu Pro Pro Asn Phe Pro Tyr Arg Asp
130 135 140
5 Asp Val Met Ser Val Asn Pro Thr Cys Leu Val Leu Ile Ile Leu Leu
145 150 155 160
Phe Ile Ser Ile Ile Leu Thr Phe Lys Gly Tyr Leu Ile Ser Cys Val
165 170 175
Trp Asn Cys Tyr Arg Tyr Ile Asn Gly Arg Asn Ser Ser Asp Val Leu
10 180 185 190
Val Tyr Val Thr Ser Asn Asp Thr Thr Val Leu Leu Pro Pro Tyr Asp
195 200 205
Asp Ala Thr Val Asn Gly Ala Ala Lys Glu Pro Pro Pro Pro Tyr Val
210 215 220
15 Ser Ala
225

<210> 93
<211> 195
20 <212> PRT
<213> Homo sapience

<400> 93
Met Arg Leu Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg
25 1 5 10 15
Ser Glu Ala Ser Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys
20 25 30
Met Gln Tyr Ala Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser
35 40 45
30 Xaa Gly Tyr Arg Arg Val Phe Glu Glu Tyr Met Arg Val Ile Ser Gln
50 55 60
Arg Tyr Pro Asp Ile Arg Ile Glu Gly Glu Asn Tyr Leu Pro Gln Pro
65 70 75 80
Ile Tyr Arg His Ile Ala Ser Phe Leu Ser Val Phe Lys Leu Val Leu
35 85 90 95

103/177

Ile Gly Leu Ile Ile Val Gly Lys Asp Pro Phe Ala Phe Phe Gly Met
 100 105 110
 Gln Ala Pro Ser Ile Trp Gln Trp Gly Gln Glu Asn Lys Val Tyr Ala
 115 120 125
 5 Cys Met Met Val Phe Phe Leu Ser Asn Met Ile Glu Asn Gln Cys Met
 130 135 140
 Ser Thr Gly Ala Phe Glu Ile Thr Leu Asn Asp Val Pro Val Trp Ser
 145 150 155 160
 Lys Leu Glu Ser Gly His Leu Pro Ser Met Gln Gln Leu Val Gln Ile
 10 165 170 175
 Leu Asp Asn Glu Met Lys Leu Asn Val His Met Asp Ser Ile Pro His
 180 185 190
 His Arg Ser
 195
 15
 <210> 94
 <211> 339
 <212> PRT
 <213> Homo sapience
 20
 <400> 94
 Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu
 1 5 10 15
 Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu
 25 20 25 30
 Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
 35 40 45
 Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
 50 55 60
 30 Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
 65 70 75 80
 Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu
 85 90 95
 Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu
 35 100 105 110

104/177

Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val Leu Gln Glu
115 120 125
Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly Met Ser Gln Arg
130 135 140
5 Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg Lys Leu Ile Glu
145 150 155 160
Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His
165 170 175
Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu
10 180 185 190
Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His
195 200 205
Ala Leu Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr
210 215 220
15 Pro Gly Ile Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn
225 230 235 240
Ile Val Glu Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn
245 250 255
Asn Gly Asp Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu
20 260 265 270
Met Leu Ile Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu
275 280 285
Gln Pro Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp
290 295 300
25 Ala Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe
305 310 315 320
Lys Ser Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys Thr
325 330 335
Lys His Asp
30
<210> 95
<211> 487
<212> PRT
<213> Homo sapience
35

105/177

<400> 95

	Met	Asp	Gly	Thr	Glu	Thr	Arg	Gln	Arg	Arg	Leu	Asp	Ser	Cys	Gly	Lys
	1					5				10					15	
	Pro	Gly	Glu	Leu	Gly	Leu	Pro	His	Pro	Leu	Ser	Thr	Gly	Gly	Leu	Pro
5				20					25						30	
	Val	Ala	Ser	Glu	Asp	Gly	Ala	Leu	Arg	Ala	Pro	Glu	Ser	Gln	Ser	Val
				35					40						45	
	Thr	Pro	Lys	Pro	Leu	Glu	Thr	Glu	Pro	Ser	Arg	Glu	Thr	Ala	Trp	Ser
				50				55						60		
10	Ile	Gly	Leu	Gln	Val	Thr	Val	Pro	Phe	Met	Phe	Ala	Gly	Leu	Gly	Leu
		65				70					75				80	
	Ser	Trp	Ala	Gly	Met	Leu	Leu	Asp	Tyr	Phe	Gln	His	Trp	Pro	Val	Phe
						85					90				95	
	Val	Glu	Val	Lys	Asp	Leu	Leu	Thr	Leu	Val	Pro	Pro	Leu	Val	Gly	Leu
15				100					105						110	
	Lys	Gly	Asn	Leu	Glu	Met	Thr	Leu	Ala	Ser	Arg	Leu	Ser	Thr	Ala	Ala
				115					120						125	
	Asn	Thr	Gly	Gln	Ile	Asp	Asp	Pro	Gln	Glu	Gln	His	Arg	Val	Ile	Ser
				130				135					140			
20	Ser	Asn	Leu	Ala	Leu	Ile	Gln	Val	Gln	Ala	Thr	Val	Val	Gly	Leu	Leu
		145				150					155				160	
	Ala	Ala	Val	Ala	Ala	Leu	Leu	Leu	Gly	Val	Val	Ser	Arg	Glu	Glu	Val
						165					170				175	
	Asp	Val	Ala	Lys	Val	Glu	Leu	Leu	Cys	Ala	Ser	Ser	Val	Leu	Thr	Ala
25				180					185					190		
	Phe	Leu	Ala	Ala	Phe	Ala	Leu	Gly	Val	Leu	Met	Val	Cys	Ile	Val	Ile
				195					200					205		
	Gly	Ala	Arg	Lys	Leu	Gly	Val	Asn	Pro	Asp	Asn	Ile	Ala	Thr	Pro	Ile
				210				215					220			
30	Ala	Ala	Ser	Leu	Gly	Asp	Leu	Ile	Thr	Leu	Ser	Ile	Leu	Ala	Leu	Val
		225				230					235				240	
	Ser	Ser	Phe	Phe	Tyr	Arg	His	Lys	Asp	Ser	Arg	Tyr	Leu	Thr	Pro	Leu
						245					250				255	
	Val	Cys	Leu	Ser	Phe	Ala	Ala	Leu	Thr	Pro	Val	Trp	Val	Leu	Ile	Ala
35				260					265						270	

106/177

Lys Gln Ser Pro Pro Ile Val Lys Ile Leu Lys Phe Gly Trp Phe Pro
 275 280 285
 Ile Ile Leu Ala Met Val Ile Ser Ser Phe Gly Gly Leu Ile Leu Ser
 290 295 300
 5 Lys Thr Val Ser Lys Gln Gln Tyr Lys Gly Met Ala Ile Phe Thr Pro
 305 310 315 320
 Val Ile Cys Gly Val Gly Gly Asn Leu Val Ala Ile Gln Thr Ser Arg
 325 330 335
 Ile Ser Thr Tyr Leu His Met Trp Ser Ala Pro Gly Val Leu Pro Leu
 10 340 345 350
 Gln Met Lys Lys Phe Trp Pro Asn Pro Cys Ser Thr Phe Cys Thr Ser
 355 360 365
 Glu Ile Asn Ser Met Ser Ala Arg Val Leu Leu Leu Leu Val Val Pro
 370 375 380
 15 Gly His Leu Ile Phe Phe Tyr Ile Ile Tyr Leu Val Glu Gly Gln Ser
 385 390 395 400
 Val Ile Asn Ser Gln Thr Phe Val Val Leu Tyr Leu Leu Ala Gly Leu
 405 410 415
 Ile Gln Val Thr Ile Leu Leu Tyr Leu Ala Glu Val Met Val Arg Leu
 20 420 425 430
 Thr Trp His Gln Ala Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu
 435 440 445
 Thr Gly Leu Gly Asp Leu Leu Gly Thr Gly Leu Leu Ala Leu Cys Phe
 450 455 460
 25 Phe Thr Asp Trp Leu Leu Lys Ser Lys Ala Glu Leu Gly Gly Ile Ser
 465 470 475 480
 Glu Leu Ala Ser Gly Pro Pro
 485
 30 <210> 96
 <211> 393
 <212> PRT
 <213> Homo sapience
 35 <400> 96

107/177

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
 1 5 10 15
 Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys
 20 25 30
 5 Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg
 35 40 45
 Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His
 50 55 60
 Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp
 10 65 70 75 80
 Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr
 85 90 95
 Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln
 100 105 110
 15 Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp
 115 120 125
 Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu
 130 135 140
 His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe
 145 150 155 160
 20 Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr
 165 170 175
 Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu
 180 185 190
 25 Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met
 195 200 205
 Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu
 210 215 220
 Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met
 225 230 235 240
 30 Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe
 245 250 255
 Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn
 260 265 270
 35 Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys

108/177

	275	280	285
	Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met		
	290	295	300
5	Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala Arg		
	305	310	315
	Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp Ser		
	325	330	335
	Gln Ala Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg		
	340	345	350
10	His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu Glu		
	355	360	365
	Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly Gln		
	370	375	380
	Gly Leu Asp Tyr Phe Tyr Asp Leu Leu		
15	385	390	
	<210> 97		
	<211> 196		
	<212> PRT		
20	<213> Homo sapience		
	<400> 97		
	Met Trp Arg Val Pro Gly Thr Thr Arg Arg Pro Val Thr Gly Glu Ser		
	1	5	10
25	Pro Gly Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala		
	20	25	30
	Leu Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly		
	35	40	45
	Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly		
30	50	55	60
	Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln Val Lys		
	65	70	75
	Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly Gly Asn Thr		
	85	90	95
35	Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr Lys Val Phe Val		

109/177

100 105 110
 Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met Tyr Thr Ser Lys Asp
 115 120 125
 Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly Gln Ile Ser Ser Ala Tyr
 5 130 135 140
 Pro Ser Gln Glu Gly Gln Val Leu Val Gly Ile Tyr Gly Gln Tyr Gln
 145 150 155 160
 Leu Leu Gly Ile Lys Ser Ile Gly Phe Glu Trp Asn Tyr Pro Leu Glu
 165 170 175
 10 Glu Pro Thr Thr Glu Pro Pro Val Asn Leu Thr Tyr Ser Ala Asn Ser
 180 185 190
 Pro Val Gly Arg
 195
 15 <210> 98
 <211> 107
 <212> PRT
 <213> Homo sapience
 20 <400> 98
 Met Glu Gln Lys Leu Val Glu Glu Ile Leu Gln Ala Ile Thr Met Ser
 1 5 10 15
 Thr Asp Thr Gly Val Ser Leu Pro Ser Tyr Glu Glu Asp Gln Gly Ser
 20 25 30
 25 Lys Leu Ile Arg Lys Ala Lys Glu Ala Pro Phe Val Pro Val Gly Ile
 35 40 45
 Ala Gly Phe Ala Ala Ile Val Ala Tyr Gly Leu Tyr Lys Leu Lys Ser
 50 55 60
 Arg Gly Asn Thr Lys Met Ser Ile His Leu Ile His Met Arg Val Ala
 30 65 70 75 80
 Ala Glu Gly Phe Val Val Gly Ala Met Thr Val Gly Met Gly Tyr Ser
 85 90 95
 Met Tyr Arg Glu Phe Trp Ala Lys Pro Lys Pro
 100 105
 35

110/177

<210> 99

<211> 350

<212> PRT

<213> Homo sapience

5

<400> 99

Met Ser Glu Val Lys Ser Arg Lys Lys Ser Gly Pro Lys Gly Ala Pro

1 5 10 15

Ala Ala Glu Pro Gly Lys Arg Ser Glu Gly Gly Lys Thr Pro Val Ala

10 20 25 30

Arg Ser Ser Gly Gly Gly Gly Trp Ala Asp Pro Arg Thr Cys Leu Ser

35 40 45

Leu Leu Ser Leu Gly Thr Cys Leu Gly Leu Ala Trp Phe Val Phe Gln

50 55 60

15 Gln Ser Glu Lys Phe Ala Lys Val Glu Asn Gln Tyr Gln Leu Leu Lys

65 70 75 80

Leu Glu Thr Asn Glu Phe Gln Gln Leu Gln Ser Lys Ile Ser Leu Ile

85 90 95

Ser Glu Lys Trp Gln Lys Ser Glu Ala Ile Met Glu Gln Leu Lys Ser

20 100 105 110

Phe Gln Ile Ile Ala His Leu Lys Arg Leu Gln Glu Glu Ile Asn Glu

115 120 125

Val Lys Thr Trp Ser Asn Arg Ile Thr Glu Lys Gln Asp Ile Leu Asn

130 135 140

25 Asn Ser Leu Thr Thr Leu Ser Gln Asp Ile Thr Lys Val Asp Gln Ser

145 150 155 160

Thr Thr Ser Met Ala Lys Asp Val Gly Leu Lys Ile Thr Ser Val Lys

165 170 175

Thr Asp Ile Arg Arg Ile Ser Gly Leu Val Thr Asp Val Ile Ser Leu

30 180 185 190

Thr Asp Ser Val Gln Glu Leu Glu Asn Lys Ile Glu Lys Val Glu Lys

195 200 205

Asn Thr Val Lys Asn Ile Gly Asp Leu Leu Ser Ser Ser Ile Asp Arg

210 215 220

35 Thr Ala Thr Leu Arg Lys Thr Ala Ser Glu Asn Ser Gln Arg Ile Asn

111/177

225 230 235 240
 Ser Val Lys Lys Thr Leu Thr Glu Leu Lys Ser Asp Phe Asp Lys His
 245 250 255
 Thr Asp Arg Phe Leu Ser Leu Glu Gly Asp Arg Ala Lys Val Leu Lys
 5 260 265 270
 Thr Val Thr Phe Ala Asn Asp Leu Lys Pro Lys Val Tyr Asn Leu Lys
 275 280 285
 Lys Asp Phe Ser Arg Leu Glu Pro Leu Val Asn Asp Leu Thr Leu Arg
 290 295 300
 10 Ile Gly Arg Leu Val Thr Asp Leu Leu Gln Arg Glu Lys Glu Ile Ala
 305 310 315 320
 Phe Leu Ser Glu Lys Ile Ser Asn Leu Thr Ile Val Gln Ala Glu Ile
 325 330 335
 Lys Asp Ile Lys Asp Glu Ile Ala His Ile Ser Asp Met Asn
 15 340 345 350

 <210> 100
 <211> 107
 <212> PRT
 20 <213> Homo sapience

 <400> 100
 Met Ser Ser Ala Gly Thr Ala Thr Pro Leu Glu Met Asp His Lys Leu
 1 5 10 15
 25 Thr Ser Gln Pro Gly Arg Pro Ser Phe Tyr Cys Asn Ser Arg His Ser
 20 25 30
 Ile Val Gly Ser Ser His Gln Leu Gly Phe Trp Phe Ser His Leu Glu
 35 40 45
 Ser Ser Gly Leu Lys Val Phe Gln Val Ser Leu Pro Cys Glu Cys Val
 30 50 55 60
 Asn Leu Pro Thr Arg Ile Ala Ser Val Val Leu Ser Leu Met Ser Leu
 65 70 75 80
 Leu Val Val Gly Gln Ala Pro Ala Trp Glu Gly Ser Leu Leu Arg Gly
 85 90 95
 35 Arg Pro Ala Gly Gly Ala His Leu Cys Ala Ala

112/177

100

105

<210> 101

<211> 1074

5 <212> DNA

<213> Homo Sapience

<400> 101

	atggctccgc	agaacctgag	caccttttgc	ctgttgctgc	tataacctcat	cggggcgggtg	60
10	attgccggac	gagattttota	taagatcttg	gggggtgcctc	gaagtgcctc	tataaaggat	120
	attaaaaagg	cctataggaa	actagccctg	cagcttcctc	ccgaccggaa	ccctgatgat	180
	ccacaagccc	aggagaaatt	ccaggatctg	ggtgctgctt	atgaggttct	gtcagatagt	240
	gagaaacgga	aacagtacga	tactttatggt	gaagaaggat	taaaagatgg	tcatcagagc	300
	tcccatggag	acattttttc	acacttcttt	ggggattttg	gtttcatgtt	tggagggaacc	360
15	cctcgtcagc	aagacagaaa	tattccaaga	ggaagtgata	ttattgtaga	tctagaagtc	420
	actttggaag	aagtatatgc	aggaaatttt	gtggaagtag	ttagaaacaa	acctgtggca	480
	aggcaggctc	ctggcaaacg	gaagtgcaat	tgtcggcaag	agatgcggac	caccagctg	540
	ggccctgggc	gcttccaaat	gaccaggag	gtggtctgctg	acgaatgccc	taatgtcaaa	600
	ctagtgaatg	aagaacgaac	gctggaagta	gaaatagagc	ctgggggtgag	agacggcatg	660
20	gagtaccctt	ttattggaga	aggtgagcct	cacgtggatg	gggagcctgg	agatttacgg	720
	ttccgaatca	aagttgtcaa	gcacccaata	tttgaaagga	gaggagatga	ttgtacaca	780
	aatgtgacaa	tctcattagt	tgagtcactg	gttggctttg	agatggatat	tactcacttg	840
	gatggtcaca	aggtacatat	ttcccgggat	aagatcacca	ggccaggagc	gaagctatgg	900
	aagaaagggg	aagggtctcc	caactttgac	aacaacaata	tcaagggctc	tttgataatc	960
25	acttttgatg	tggattttcc	aaaagaacag	ttaacagagg	aagcgagaga	aggtatcaaa	1020
	cagctactga	aacaagggtc	agtgcagaag	gtatacaatg	gactgcaagg	atat	1074

<210> 102

<211> 678

30 <212> DNA

<213> Homo Sapience

<400> 102

	atgaagatgg	tcgcgccttg	gacgcgggtc	tactccaaca	gctgctgctt	gtgetgcoat	60
35	gtccgcaccg	gcaccatcct	gctcggcgctc	tggtatctga	tcataaatgc	tgtgggtactg	120

113/177

5 ttgattttat tgagtgcct ggctgatccg gatcagtata acttttcaag ttctgaactg 180
 ggaggtgact ttgagttcat ggatgatgcc aacatgtgca ttgccattgc gattttctctt 240
 ctcatgatcc tgatatgtgc tatggctact tacggagcgt acaagcaacg cgcagcctgg 300
 atcatcccat tcttctgtta ccagatcttt gactttgccc tgaacatggt gggtgcaatc 360
 actgtgetta tttatccaaa ctccattcag gaatacatat ggcaactgcc tcttaatttt 420
 ccctacagag atgatgtcat gtcagtgaat cctacctgtt tggtccttat tattcttctg 480
 tttattagca ttatcttgac ttttaagggt tacttgatta gctgtgtttg gaactgctac 540
 cgatacatca atggtaggaa ctctctgat gtctgtgttt atgttaccag caatgacact 600
 acggtgetgc taccctcgta tgatgatgcc actgtgaatg gtgctgccaa ggagccaccg 660
 10 ccaccttaacg tgtctgcc 678

<210> 103

<211> 585

<212> DNA

15 <213> Homo Sapience

<400> 103

20 atgaggettc tgetgettct cctagtggcg gcgtctgcga tggtcgggag cgaggcctcg 60
 gccaatctgg gcggcgtgcc cagcaagaga ttaaagatgc agtacgccac ggggccgctg 120
 ctcaagttcc agattttgtgt ttcttgaggt tataggcggg tgtttgagga gtacatgcgg 180
 gttattagcc agcggtagcc agacatccgc attgaaggag agaattacct cctcaacca 240
 atatatagac acatagcatc ttctctgtca gtcttcaaac tagtattaat aggettaata 300
 attgttggca aggatccttt tgctttcttt ggcatgcaag ctcttagcat ctggcagtgg 360
 ggccaagaaa ataaggttta tgcattgtat atggttttct tcttgagcaa catgattgag 420
 25 aaccagtgta tgtcaacagg tgcatttgag ataacttta atgatgtacc tgtgtggtct 480
 aagctggaat ctggtcacct tccatccatg caacaacttg ttcaaattct tgacaatgaa 540
 atgaagctca atgtgcatat ggattcaatc ccacaccatc gatca 585

<210> 104

30 <211> 1017

<212> DNA

<213> Homo Sapience

<400> 104

35 atgaactggg agctgctgct gtggctgctg gtgctgtgcg cgctgctcct gctcttggtg 60

114/177

5 cagctgctgc gcttcctgag ggctgacggc gacctgacgc tactatgggc cgagtggcag 120
 ggacgacgcc cagaatggga gctgactgat atgggtggtg gggtgactgg agcctcgagt 180
 ggaattggtg aggagctggc ttaccagttg tctaaactag gagtttctct tgtgctgtca 240
 gccagaagag tgcattgagct ggaaaggggtg aaaagaagat gcctagagaa tggcaattta 300
 aaagaaaaag atatacttgt tttgcccctt gacctgaccg aacttggttc ccatgaagcg 360
 gctaccaaag ctgttctcca ggagtttggg agaactgaca ttctggtcaa caatggtgga 420
 atgtcccagc gttctctgtg catggatacc agcttggtat tctacagaaa gctaatagag 480
 cttaactact tagggacggg gtccttgaca aaatgtgttc tgctcacat gatcgagagg 540
 aagcaaggaa agattgttac tgtgaatagc atcctgggta tcatatctgt acctctttcc 600
 10 attggatact gtgctagcaa gcatgctctc cggggttttt ttaatggcct tcgaacagaa 660
 cttgccacat acccagggtat aatagtttct aacatttgcc caggacctgt gcaatcaaata 720
 attgtggaga attccctagc tggagaagtc acaaagacta taggcaataa tggagaccag 780
 tcccacaaga tgacaaccag tcgttgtgtg cggctgatgt taatcagcat ggccaatgat 840
 ttgaaagaag tttggatctc agaacaacct ttcttgttag taacatattt gtggcaatac 900
 15 atgccaacct gggcctggtg gataaccaac aagatgggga agaaaaggat tgagaacttt 960
 aagagtgggtg tggatgcaga ctcttcttat ttaaaatct ttaagacaaa acatgac 1017

<210> 105

<211> 1461

20 <212> DNA

<213> Homo Sapiens

<400> 105

25 atggatggga cagagacccg gcagcggagg ctggacagct gtggcaagcc aggggagctg 60
 gggcttcctc accccctcag cacaggagga ctccctgtag cctcagaaga tggagctctc 120
 agggcccctg agagccaaaag cgtgaccccc aagccactgg agactgagcc tagcagggag 180
 accgcctggt ccataggcct tcaggtgacc gtgcccttca tgtttgcagg cctgggactg 240
 tcttgggccc gcatgcttct ggactatttc cagcactggc ctgtgtttgt ggaggtgaaa 300
 gaccttttga cattggtgcc gccctggtg ggctgaagg ggaacctgga gatgacactg 360
 30 gcatccagac tctccacagc tgccaacact ggacaaattg atgaccccca ggagcagcac 420
 agagtcacat gcagcaacct ggccctcctc caggtgcagg cactgtcgt ggggctcttg 480
 gctgctgtgg ctgcctgct gttgggcgtg gtgtctcgag aggaagtgga tgtgccaaag 540
 gtggagttgc tgtgtgccag cagtgtctc actgccttcc ttgcagcctt tgccctgggg 600
 gtgctgatgg tctgtatagt gattggtgct cgaaagctcg gggtaacccc agacaacatt 660
 35 gccacgcccc ttgcagccag cctgggagac ctcatcacac tgtccattct ggctttggtt 720

115/177

	agcagcttct tctacagaca caaagatagt cggatatctga cgccgctggt ctgcctcagc	780
	tttgcggtct tgaccccagt gtgggtcctc attgccaagc agagcccacc catcgtgaag	840
	atcctgaagt ttggttggtt cccaatcatc ctggccatgg tcatcagcag ttccggagga	900
	ctcatcttga gcaaaaccgt ttctaaacag cagtacaaag gcatggcgat atttaccccc	960
5	gtcatatgtg gtgttggtgg caatctggtg gccattcaga ccagccgaat ctcaacctac	1020
	ctgcacatgt ggagtgcacc tggcgtcctg cccctccaga tgaagaaatt ctggcccaac	1080
	ccgtgttcta ctttctgcac gtcagaaatc aattccatgt cagctcgagt cctgctcttg	1140
	ctggttggtcc caggccatct gattttcttc tacatcatct acctgggtgga gggtcagtca	1200
	gtcataaaca gccagacctt tgtggtgctc tacctgctgg caggcctgat ccaggtgaca	1260
10	atcctgctgt acctggcaga agtgatggtt cggtgactt ggcaccaggc cctggatcct	1320
	gacaaccact gcaccccta ccttacaggg ctgggggacc tgcctgggtac tggcctcctg	1380
	gcactctgct ttttactga ctggctactg aagagcaagg cagagctggg tggcatctca	1440
	gaactggcat ctggacctcc c	1461
15	<210> 106	
	<211> 1179	
	<212> DNA	
	<213> Homo Sapience	
20	<400> 106	
	atgcggacac tcttcaacct cctctggctt gccctggcct gcagccctgt tcacactacc	60
	ctgtcaaagt cagatgccaa aaaagccgcc tcaaagacgc tgcctggagaa gagtcagttt	120
	tcagataagc cgggtgcaaga ccgggggttg gtggtgacgg acctcaaagc tgagagtgtg	180
	gttcttgagc atcgcagcta ctgctcgga aaggcccgga acagacactt tgctggggat	240
25	gtactgggct atgtcactcc atggaacagc catggctacg atgtcaccaa ggtctttggg	300
	agcaagttca cacagatctc acccgtctgg ctgcagctga agagacgtgg ccgtgagatg	360
	tttgaggtea cgggcctcca cgacgtggac caagggtgga tgcgagctgt caggaagcat	420
	gccaaaggcc tgcacatagt gcctcggtc ctgtttgagg actggactta cgatgatttc	480
	cggaacgtct tagacagtga ggatgagata gaggagctga gcaagaccgt ggtccagggtg	540
30	gcaaaagaacc agcatttoga tggcttcgtg gtggaggtct ggaaccagct gctaagccag	600
	aagcgcgtgg gcctcatcca catgctcacc cacttgccg aggctctgca ccaggcccg	660
	ctgctggccc tcctggteat cccgcctgcc atcaccccg ggaccgacca gctgggcatg	720
	ttcacgcaca aggagtttga gcagctggcc cccgtgctgg atggtttcag cctcatgacc	780
	tacgactact ctacagcgca tcagcctggc cctaatacac ccctgtcctg ggttcagacc	840
35	tgcgtccagg tcctggaccc gaagtccaag tggcgaagca aaatcctcct ggggctcaac	900

116/177

	ttctatggta tggactacgc gacctccaag gatgcccggtg agcctgttgt cggggccagg	960
	tacatccaga cactgaagga ccacaggccc cggatggtgt gggacagcca ggcctcagag	1020
	cacttcttcg agtacaagaa gagccgcagt gggaggcacg tcgtcttcta cccaacctg	1080
	aagtccttgc aggtgcggct ggagctggcc cgggagctgg gcgttgggggt ctctatctgg	1140
5	gagctggggc agggcctgga ctacttctac gacctgtc	1179
	<210> 107	
	<211> 588	
	<212> DNA	
10	<213> Homo Sapience	
	<400> 107	
	atgtggaggg tgcccggcac aaccagacgc ccagtcacag gcgagagccc tgggatgcac	60
	cgccagagg ccatgctgct gctgctcacg cttgccctcc tggggggccc cacctgggca	120
15	gggaagatgt atggccctgg aggaggcaag tatttcagca cactgaaga ctacgacct	180
	gaaatcacag ggctgcgggt gtctgtaggt cttctcctgg tgaaaagtgt ccaggtgaaa	240
	cttgagact cctgggacgt gaaactggga gccttaggtg ggaataccca ggaagtcacc	300
	ctgcagccag gcgaatacat cacaaaagtc tttgtcgct tccaagcttt cctccgggggt	360
	atggtcattg acaccagcaa ggaccgctat ttctattttg ggaagcttga tggccagatc	420
20	tcctctgcct accccagcca agaggggcag gtgctggtgg gcatttatgg ccagtatcaa	480
	ctccttggca tcaagagcat tggctttgaa tggaattatc cactagagga gccgaccact	540
	gagccaccag ttaatctcac atactcagca aactcaccgc tgggtcgc	588
	<210> 108	
25	<211> 321	
	<212> DNA	
	<213> Homo Sapience	
	<400> 108	
30	atggagcaga agcttgtgga ggagattctt caagcaatca ctatgtcaac agacacaggt	60
	gtttcccttc cttcatatga ggaagatcag ggatcaaac tcattcgaaa agctaaagag	120
	gcaccattcg taccggttgg aatagcgggt tttgcagcaa ttgttgcata tggattatat	180
	aaactgaaga gcaggggaaa tactaaaatg tccattcatt tgatccacat gcgtgtggca	240
	gcccagggct ttgttgtagg agcaatgact gttggtatgg gctattccat gtatcgggaa	300
35	ttctgggcaa aacctagcc t	321

117/177

<210> 109

<211> 1050

<212> DNA

5 <213> Homo Sapience

<400> 109

	atgtctgagg tgaagagccg gaagaagtcg gggcccaagg gagccctgc tgcggagccc	60
	gggaagcggg gcgagggcgg gaagaccccc gtggcccggg gcagcggagg cgggggctgg	120
10	gcagaccccc gaacgtgcct gagcctgctg tcgctgggga cgtgcctggg cctggcctgg	180
	tttgtatttc agcagtcaga aaaatttgca aaggtggaaa accaatacca gttactgaaa	240
	ctagaaacca atgaattcca acaacttcaa agtaaaatca gtttaatttc agaaaagtgg	300
	cagaaatctg aagctatcat ggaacaattg aagtcttttc aaataattgc tcactataag	360
	cgtctacagg aagaaattaa tgaggtaaaa acttggtcca ataggataac tgaaaaacag	420
15	gatatactga acaacagtct gacgacgctt tctcaagaca ttacaaaagt agaccaaagt	480
	acaacttcca tggcaaaaga tggttggtctc aagattacaa gtgtaaaaac agatatacga	540
	cggatttcag gtttagtaac tgatgtaata tcattgacag attctgtgca agaactagaa	600
	aataaaatag agaaagtaga aaaaaataca gtaaaaaata taggtgatct tctttcaagc	660
	agtattgatc gaacagcaac gctccgaaag acagcatctg aaaattcaca agaattaac	720
20	tctgttaaga agacgctaac cgaactaaag agtgacttcg acaaacatac agatagattt	780
	ctaagcttag aaggtgacag agccaaagtt ctgaagacag tgacttttgc aaatgatcta	840
	aaaccaaaagg tgtataatct aaagaaggac ttttcccggt tagaaccatt agtaaattgat	900
	ttaacactac gcattgggag attggttacc gacttactac aaagagagaa agaaattgct	960
	ttcttaagtg aaaaaatata taatttaaca atagtccaag ctgagattaa ggatattaaa	1020
25	gatgaaatag cacacatttc agatatgaat	1050

<210> 110

<211> 321

<212> DNA

30 <213> Homo Sapience

<400> 110

	atgtcctcag caggcacagc aaccctctctg gaaatggatc acaaactcac ttctcagcca	60
	ggcaggccaa gcttctattg taacagtagg cacagtatag tcggatcatc acatcagctg	120
35	ggtttttggg ttagtcatct agagtctgtt ggactaaagg tctttcaggt ctcttggccc	180

118/177

tgtgagtgcg tgaacctccc caccgaatt gcctcagttg tctgagcct catgtctctc 240
 ctggtggtgg gccaggcccc tgcattgggaa gggagcctgc tgcggggcag gccagctggg 300
 ggtgctcacc tatgcgcagc a 321

5 <210> 111
 <211> 1619
 <212> DNA
 <213> Homo Sapiens
 <220>

10 <221> CDS
 <222> (158)...(1234)

<400> 111
 agaagagggg gctagctagc tgtctctgcg gaccagggag acccccgccg ccccccggtg 60
 15 tgaggcggcc tcacagggcc ggggtgggctg gcgagccgac gcggcggcgg aggaggctgt 120
 gaggagtgtg tggaacagga cccgggacag aggaacc atg gct ccg cag aac ctg 175
 Met Ala Pro Gln Asn Leu
 1 5

20 agc acc ttt tgc ctg ttg ctg cta tac ctc atc ggg gcg gtg att gcc 223
 Ser Thr Phe Cys Leu Leu Leu Leu Tyr Leu Ile Gly Ala Val Ile Ala
 10 15 20
 gga cga gat ttc tat aag atc ttg ggg gtg cct cga agt gcc tct ata 271
 Gly Arg Asp Phe Tyr Lys Ile Leu Gly Val Pro Arg Ser Ala Ser Ile
 25 30 35

25 aag gat att aaa aag gcc tat agg aaa cta gcc ctg cag ctt cat ccc 319
 Lys Asp Ile Lys Lys Ala Tyr Arg Lys Leu Ala Leu Gln Leu His Pro
 40 45 50

30 gac cgg aac cct gat gat cca caa gcc cag gag aaa ttc cag gat ctg 367
 Asp Arg Asn Pro Asp Asp Pro Gln Ala Gln Glu Lys Phe Gln Asp Leu
 55 60 65 70
 ggt gct gct tat gag gtt ctg tca gat agt gag aaa cgg aaa cag tac 415
 Gly Ala Ala Tyr Glu Val Leu Ser Asp Ser Glu Lys Arg Lys Gln Tyr
 75 80 85

35 gat act tat ggt gaa gaa gga tta aaa gat ggt cat cag agc tcc cat 463
 Asp Thr Tyr Gly Glu Glu Gly Leu Lys Asp Gly His Gln Ser Ser His

119/177

	90	95	100	
	gga gac att ttt tca cac ttc ttt ggg gat ttt ggt ttc atg ttt gga			511
	Gly Asp Ile Phe Ser His Phe Phe Gly Asp Phe Gly Phe Met Phe Gly			
	105	110	115	
5	gga acc cct cgt cag caa gac aga aat att cca aga gga agt gat att			559
	Gly Thr Pro Arg Gln Gln Asp Arg Asn Ile Pro Arg Gly Ser Asp Ile			
	120	125	130	
	att gta gat cta gaa gtc act ttg gaa gaa gta tat gca gga aat ttt			607
	Ile Val Asp Leu Glu Val Thr Leu Glu Glu Val Tyr Ala Gly Asn Phe			
10	135	140	145	150
	gtg gaa gta gtt aga aac aaa cct gtg gca agg cag gct cct ggc aaa			655
	Val Glu Val Val Arg Asn Lys Pro Val Ala Arg Gln Ala Pro Gly Lys			
	155	160	165	
	cgg aag tgc aat tgt cgg caa gag atg cgg acc acc cag ctg ggc cct			703
15	Arg Lys Cys Asn Cys Arg Gln Glu Met Arg Thr Thr Gln Leu Gly Pro			
	170	175	180	
	ggg cgc ttc caa atg acc cag gag gtg gtc tgc gac gaa tgc cct aat			751
	Gly Arg Phe Gln Met Thr Gln Glu Val Val Cys Asp Glu Cys Pro Asn			
	185	190	195	
20	gtc aaa cta gtg aat gaa gaa cga acg ctg gaa gta gaa ata gag cct			799
	Val Lys Leu Val Asn Glu Glu Arg Thr Leu Glu Val Glu Ile Glu Pro			
	200	205	210	
	ggg gtg aga gac ggc atg gag tac ccc ttt att gga gaa ggt gag cct			847
	Gly Val Arg Asp Gly Met Glu Tyr Pro Phe Ile Gly Glu Gly Glu Pro			
25	215	220	225	230
	cac gtg gat ggg gag cct gga gat tta cgg ttc cga atc aaa gtt gtc			895
	His Val Asp Gly Glu Pro Gly Asp Leu Arg Phe Arg Ile Lys Val Val			
	235	240	245	
	aag cac cca ata ttt gaa agg aga gga gat gat ttg tac aca aat gtg			943
30	Lys His Pro Ile Phe Glu Arg Arg Gly Asp Asp Leu Tyr Thr Asn Val			
	250	255	260	
	aca atc tca tta gtt gag tca ctg gtt ggc ttt gag atg gat att act			991
	Thr Ile Ser Leu Val Glu Ser Leu Val Gly Phe Glu Met Asp Ile Thr			
	265	270	275	
35	cac ttg gat ggt cac aag gta cat att tcc cgg gat aag atc acc agg			1039

120/177

	His Leu Asp Gly His Lys Val His Ile Ser Arg Asp Lys Ile Thr Arg	
	280 285 290	
	cca gga gcg aag cta tgg aag aaa ggg gaa ggg ctc ccc aac ttt gac	1087
	Pro Gly Ala Lys Leu Trp Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp	
5	295 300 305 310	
	aac aac aat atc aag ggc tct ttg ata atc act ttt gat gtg gat ttt	1135
	Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe	
	315 320 325	
	cca aaa gaa cag tta aca gag gaa gcg aga gaa ggt atc aaa cag cta	1183
10	Pro Lys Glu Gln Leu Thr Glu Glu Ala Arg Glu Gly Ile Lys Gln Leu	
	330 335 340	
	ctg aaa caa ggg tca gtg cag aag gta tac aat gga ctg caa gga tat	1231
	Leu Lys Gln Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr	
	345 350 355	
15	tgagagtga ataaaattgg actttgttta aaataagtga ataagcgata tttattatct	1290
	gcaagggtttt tttgtgtgtg tttttgtttt tattttcaat atgcaagtta ggcttaattt	1350
	ttttatctaa tgatcatcat gaaatgaata agagggctta agaatttgtc catttgcatt	1410
	cggaaaagaa tgaccagcaa aaggtttact aatacctctc cctttgggga tttaatgtct	1470
	ggtgctgcgc cctgagtttc aagaattaaa gctgcaagag gactccagga gcaaaagaaa	1530
20	cacaatatag aggggttgag ttgtagcaa tttcattcaa aatgccaaact ggagaagtct	1590
	gtttttaaat acattttgtt gttattttt	1619
	<210> 112	
	<211> 2054	
25	<212> DNA	
	<213> Homo Sapience	
	<220>	
	<221> CDS	
	<222> (254)...(934)	
30	<400> 112	
	cacatggcca agtccgcccc gccccctccc cgcccccgcc gctgcagcgg tcgccttcgg	60
	agcgaagggt accgacccgg cagaagctcg gagctctcgg ggtatcgagg aggcaggccc	120
	gcggggcgac gggcgagcgg gccgggagcc ggagcggcgg aggagccggc agcagcggcg	180
35	cgggcggtc caggcgaggc ggtcgacgct cctgaaaact tgcgcgcgcg ctgcgcgccac	240

121/177

	tgcgcgcgga gcg atg aag atg gtc gcg ccc tgg acg cgg ttc tac tcc	289
	Met Lys Met Val Ala Pro Trp Thr Arg Phe Tyr Ser	
	1 5 10	
	aac agc tgc tgc ttg tgc tgc cat gtc cgc acc ggc acc atc ctg ctc	337
5	Asn Ser Cys Cys Leu Cys Cys His Val Arg Thr Gly Thr Ile Leu Leu	
	15 20 25	
	ggc gtc tgg tat ctg atc atc aat gct gtg gta ctg ttg att tta ttg	385
	Gly Val Trp Tyr Leu Ile Ile Asn Ala Val Val Leu Leu Ile Leu Leu	
	30 35 40	
10	agt gcc ctg gct gat ccg gat cag tat aac ttt tca agt tct gaa ctg	433
	Ser Ala Leu Ala Asp Pro Asp Gln Tyr Asn Phe Ser Ser Ser Glu Leu	
	45 50 55 60	
	gga ggt gac ttt gag ttc atg gat gat gcc aac atg tgc att gcc att	481
	Gly Gly Asp Phe Glu Phe Met Asp Asp Ala Asn Met Cys Ile Ala Ile	
15	65 70 75	
	gcg att tct ctt ctc atg atc ctg ata tgt gct atg gct act tac gga	529
	Ala Ile Ser Leu Leu Met Ile Leu Ile Cys Ala Met Ala Thr Tyr Gly	
	80 85 90	
	gcg tac aag caa cgc gca gcc tgg atc atc cca ttc ttc tgt tac cag	577
20	Ala Tyr Lys Gln Arg Ala Ala Trp Ile Ile Pro Phe Phe Cys Tyr Gln	
	95 100 105	
	atc ttt gac ttt gcc ctg aac atg ttg gtt gca atc act gtg ctt att	625
	Ile Phe Asp Phe Ala Leu Asn Met Leu Val Ala Ile Thr Val Leu Ile	
	110 115 120	
25	tat cca aac tcc att cag gaa tac ata cgg caa ctg cct cct aat ttt	673
	Tyr Pro Asn Ser Ile Gln Glu Tyr Ile Arg Gln Leu Pro Pro Asn Phe	
	125 130 135 140	
	ccc tac aga gat gat gtc atg tca gtg aat cct acc tgt ttg gtc ctt	721
	Pro Tyr Arg Asp Asp Val Met Ser Val Asn Pro Thr Cys Leu Val Leu	
30	145 150 155	
	att att ctt ctg ttt att agc att atc ttg act ttt aag ggt tac ttg	769
	Ile Ile Leu Leu Phe Ile Ser Ile Ile Leu Thr Phe Lys Gly Tyr Leu	
	160 165 170	
	att agc tgt gtt tgg aac tgc tac cga tac atc aat ggt agg aac tcc	817
35	Ile Ser Cys Val Trp Asn Cys Tyr Arg Tyr Ile Asn Gly Arg Asn Ser	

122/177

	175	180	185	
	tet gat gtc ctg gtt tat gtt acc agc aat gac act acg gtg ctg cta			865
	Ser Asp Val Leu Val Tyr Val Thr Ser Asn Asp Thr Thr Val Leu Leu			
	190	195	200	
5	ccc ccg tat gat gat gcc act gtg aat ggt gct gcc aag gag cca ccg			913
	Pro Pro Tyr Asp Asp Ala Thr Val Asn Gly Ala Ala Lys Glu Pro Pro			
	205	210	215	220
	cca cct tac gtg tct gcc taagccttca agtgggcgga gctgagggc			960
	Pro Pro Tyr Val Ser Ala			
10	225			
	agcagcttga ctttgcagac atctgagcaa tagttctgtt atttcacttt tgccatgagc			1020
	ctctctgagc ttgtttgttg ctgaaatgct actttttaaa atttagatgt tagattgaaa			1080
	actgtagttt tcaacatatg ctttgctgga acactgtgat agattaactg tagaattcct			1140
	cctgtacgat tggggatata atgggettca ctaaccttcc ctaggcattg aaacttcccc			1200
15	caaattctgat ggacctagaa gtctgctttt gtacctgctg ggccccaag ttgggcattt			1260
	ttctctctgt tccctctctt ttgaaaatgt aaaataaaac caaaaataga caacttttct			1320
	ttcagccatt ccagcataga gaacaaaacc ttatggaaac aggaatgtca attgtgtaat			1380
	cattgtttcta attaggtaaa tagaagtcct tatgtatgtg ttacaagaat ttccccaca			1440
	acatccttta tgactgaagt tcaatgacag tttgtgtttg gtggtaaagg attttctcca			1500
20	tggcctgaat taagaccatt agaaagcacc aggccgtggg agcagtgacc atctgctgac			1560
	tggtctgtgt gatcttgtgt ccagggacat ggggtgacat gctctgtatg tgtagaggg			1620
	tggaatggat gtgtttggcg ctgcatggga tctggtgcc ctcttctcct ggattcacat			1680
	ccccaccag ggcgcgttt tactaagtgt tctgccctag attggttcaa ggaggtcatc			1740
	caactgactt tatcaagtgg aattgggata tatttgatat acttctgcct aacaacatgg			1800
25	aaaagggttt tcttttccct gcaagctaca tctactgct ttgaacttcc aagtatgtct			1860
	agtcaccttt taaaatgtaa acattttcag aaaaatgagg attgccttcc ttgtatgcgc			1920
	tttttacctt gactacctga attgcaaggg atttttatat attcatatgt taaaaagtca			1980
	gcaactctcc tgttggttca ttattgaatg tgctgtaaata taagttgttt gcaattaaaa			2040
	caaggtttgc ccac			2054
30				
	<210> 113			
	<211> 1380			
	<212> DNA			
	<213> Homo Sapiens			
35	<220>			

123/177

<221> CDS

<222> (43)...(630)

<400> 113

5	gcagtcctgtc tgagggcggc cgaagtggct ggctcattta ag atg agg ctt ctg	54
	Met Arg Leu Leu	
	1	
	ctg ctt ctc cta gtg gcg gcg tct gcg atg gtc cgg agc gag gcc tcg	102
	Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg Ser Glu Ala Ser	
10	5 10 15 20	
	gcc aat ctg ggc ggc gtg ccc agc aag aga tta aag atg cag tac gcc	150
	Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys Met Gln Tyr Ala	
	25 30 35	
	acg ggg ccg ctg ctc aag ttc cag att tgt gtt tcc tga ggt tat agg	198
15	Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser Xaa Gly Tyr Arg	
	40 45 50	
	cgg gtg ttt gag gag tac atg cgg gtt att agc cag cgg tac cca gac	246
	Arg Val Phe Glu Glu Tyr Met Arg Val Ile Ser Gln Arg Tyr Pro Asp	
	55 60 65	
20	atc cgc att gaa gga gag aat tac ctc cct caa cca ata tat aga cac	294
	Ile Arg Ile Glu Gly Glu Asn Tyr Leu Pro Gln Pro Ile Tyr Arg His	
	70 75 80	
	ata gca tct ttc ctg tca gtc ttc aaa cta gta tta ata ggc tta ata	342
	Ile Ala Ser Phe Leu Ser Val Phe Lys Leu Val Leu Ile Gly Leu Ile	
25	85 90 95 100	
	att gtt ggc aag gat cct ttt gct ttc ttt ggc atg caa gct cct agc	390
	Ile Val Gly Lys Asp Pro Phe Ala Phe Phe Gly Met Gln Ala Pro Ser	
	105 110 115	
	atc tgg cag tgg ggc caa gaa aat aag gtt tat gca tgt atg atg gtt	438
30	Ile Trp Gln Trp Gly Gln Glu Asn Lys Val Tyr Ala Cys Met Met Val	
	120 125 130	
	ttc ttc ttg agc aac atg att gag aac cag tgt atg tca aca ggt gca	486
	Phe Phe Leu Ser Asn Met Ile Glu Asn Gln Cys Met Ser Thr Gly Ala	
	135 140 145	
35	ttt gag ata act tta aat gat gta cct gtg tgg tct aag ctg gaa tct	534

124/177

	Phe Glu Ile Thr Leu Asn Asp Val Pro Val Trp Ser Lys Leu Glu Ser	
	150 155 160	
	ggt cac ctt cca tcc atg caa caa ctt gtt caa att ctt gac aat gaa	582
	Gly His Leu Pro Ser Met Gln Gln Leu Val Gln Ile Leu Asp Asn Glu	
5	165 170 175 180	
	atg aag ctc aat gtg cat atg gat tca atc cca cac cat cga tca	627
	Met Lys Leu Asn Val His Met Asp Ser Ile Pro His His Arg Ser	
	185 190 195	
	tag caccacctat cagcactgaa aactcttttg cattaaggga tcattgcaag	680
10	agcagcgtga ctgacattat gaaggcctgt actgaagaca gcaagctgtt agtacagacc	740
	agatgctttc ttggcaggct cgttgtagct cttggaaaac ctcaatgcaa gatagtgttt	800
	cagtgtctggc atatttttga attctgcaca ttcattggagt gcaataatac tgtatagctt	860
	ccccacctc ccacaaaatc acccagttaa tgtgtgtgtg tgtttttttt ttttaaggtaa	920
	acattactac ttgtaaactt ttttcttagt catatttgaa aaagtagaaa attgagttac	980
15	aatttgattt tttttccaaa gatgtctgtt aaatctgttg tgcttttata tgaatatttg	1040
	ttttttatag tttaaaattg atcctttggg aatccagttg aagttcccaa atactttata	1100
	agagtttatc agacatctct aatttggcca tgtccagttt atacagttta caaaatatag	1160
	cagatgcaag attatggggg aaatcctata ttcagagtac tctataaatt tttgtgtatg	1220
	tgtgtatgtg cgtgtgatta ccagagaact actaaaaaaa ccaactgctt tttaaatcct	1280
20	attgtgtagt taaagtgtca tgccttgacc aatctaataa attgattaat taactgggcc	1340
	tttatactta actaaataaa aaactaagca gatatgagtt	1380
	<210> 114	
	<211> 1292	
25	<212> DNA	
	<213> Homo Sapience	
	<220>	
	<221> CDS	
	<222> (113)...(1132)	
30	<400> 114	
	aaaagtgcgg ctctgggctg gcgaagggg tggcgtgcg atcccgagg gcagcgacgc	60
	gactctgggtg cgggcgctct tcttcccccc gagetgggag tgcgcggccg ca atg aac	118
	Met Asn	
35	1	

125/177

	tgg gag ctg ctg ctg tgg ctg ctg gtg ctg tgc gcg ctg ctc ctg ctc	166
	Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu Leu	
	5 10 15	
5	ttg gtg cag ctg ctg cgc ttc ctg agg gct gac ggc gac ctg acg cta	214
	Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu Thr Leu	
	20 25 30	
	cta tgg gcc gag tgg cag gga cga cgc cca gaa tgg gag ctg act gat	262
	Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu Thr Asp	
	35 40 45 50	
10	atg gtg gtg tgg gtg act gga gcc tcg agt gga att ggt gag gag ctg	310
	Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu Leu	
	55 60 65	
	gct tac cag ttg tct aaa cta gga gtt tct ctt gtg ctg tca gcc aga	358
	Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser Ala Arg	
15	70 75 80	
	aga gtg cat gag ctg gaa agg gtg aaa aga aga tgc cta gag aat ggc	406
	Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu Asn Gly	
	85 90 95	
	aat tta aaa gaa aaa gat ata ctt gtt ttg ccc ctt gac ctg acc gac	454
20	Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu Thr Asp	
	100 105 110	
	act ggt tcc cat gaa gcg gct acc aaa gct gtt ctc cag gag ttt ggt	502
	Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val Leu Gln Glu Phe Gly	
	115 120 125 130	
25	aga atc gac att ctg gtc aac aat ggt gga atg tcc cag cgt tct ctg	550
	Arg Ile Asp Ile Leu Val Asn Asn Gly Gly Met Ser Gln Arg Ser Leu	
	135 140 145	
	tgc atg gat acc agc ttg gat gtc tac aga aag cta ata gag ctt aac	598
	Cys Met Asp Thr Ser Leu Asp Val Tyr Arg Lys Leu Ile Glu Leu Asn	
30	150 155 160	
	tac tta ggg acg gtg tcc ttg aca aaa tgt gtt ctg cct cac atg atc	646
	Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His Met Ile	
	165 170 175	
	gag agg aag caa gga aag att gtt act gtg aat agc atc ctg ggt atc	694
35	Glu Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu Gly Ile	

126/177

	180	185	190	
	ata tct gta cct ctt tcc att gga tac tgt gct agc aag cat gct ctc			742
	Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His Ala Leu			
	195	200	205	210
5	cgg ggt ttt ttt aat ggc ctt cga aca gaa ctt gcc aca tac cca ggt			790
	Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly			
		215	220	225
	ata ata gtt tct aac att tgc cca gga cct gtg caa tca aat att gtg			838
	Ile Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val			
10		230	235	240
	gag aat tcc cta gct gga gaa gtc aca aag act ata ggc aat aat gga			886
	Glu Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly			
		245	250	255
	gac cag tcc cac aag atg aca acc agt cgt tgt gtg cgg ctg atg tta			934
15	Asp Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu			
		260	265	270
	atc agc atg gcc aat gat ttg aaa gaa gtt tgg atc tca gaa caa cct			982
	Ile Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro			
		275	280	285
20	ttc ttg tta gta aca tat ttg tgg caa tac atg cca acc tgg gcc tgg			1030
	Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala Trp			
		295	300	305
	tgg ata acc aac aag atg ggg aag aaa agg att gag aac ttt aag agt			1078
	Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe Lys Ser			
25		310	315	320
	ggt gtg gat gca gac tct tct tat ttt aaa atc ttt aag aca aaa cat			1126
	Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys Thr Lys His			
		325	330	335
	gac tgaaaagagc atctgtactt ttcaagccac tggagggaaa aatggaaaac a			1180
30	Asp			
	tgaaaacagc aatctttctta tgcttctgaa taatcaaaga ctaatttgtg gttttacttt			1240
	ttaatatagata tgacttttgc tccaacatgg aatgaaataa aaaataagta at			1292
35	<210> 115			

127/177

<211> 2168

<212> DNA

<213> Homo Sapience

<220>

5 <221> CDS

<222> (56)...(1519)

<400> 115

	tttccgccgc cgcctgggag gggaccocggg ctgccaggcg cccagctgtg cccag	55
10	atg gat ggg aca gag acc cgg cag cgg agg ctg gac agc tgt ggc aag	103
	Met Asp Gly Thr Glu Thr Arg Gln Arg Arg Leu Asp Ser Cys Gly Lys	
	1 5 10 15	
	cca ggg gag ctg ggg ctt cct cac ccc ctc agc aca gga gga ctc cct	151
	Pro Gly Glu Leu Gly Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro	
15	20 25 30	
	gta gcc tca gaa gat gga gct ctc agg gcc cct gag agc caa agc gtg	199
	Val Ala Ser Glu Asp Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val	
	35 40 45	
	acc ccc aag cca ctg gag act gag cct agc agg gag acc gcc tgg tcc	247
20	Thr Pro Lys Pro Leu Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser	
	50 55 60	
	ata ggc ctt cag gtg acc gtg ccc ttc atg ttt gca ggc ctg gga ctg	295
	Ile Gly Leu Gln Val Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu	
	65 70 75 80	
25	tcc tgg gcc ggc atg ctt ctg gac tat ttc cag cac tgg cct gtg ttt	343
	Ser Trp Ala Gly Met Leu Leu Asp Tyr Phe Gln His Trp Pro Val Phe	
	85 90 95	
	gtg gag gtg aaa gac ctt ttg aca ttg gtg ccg ccc ctg gtg ggc ctg	391
	Val Glu Val Lys Asp Leu Leu Thr Leu Val Pro Pro Leu Val Gly Leu	
30	100 105 110	
	aag ggg aac ctg gag atg aca ctg gca tcc aga ctc tcc aca gct gcc	439
	Lys Gly Asn Leu Glu Met Thr Leu Ala Ser Arg Leu Ser Thr Ala Ala	
	115 120 125	
	aac act gga caa att gat gac ccc cag gag cag cac aga gtc atc agc	487
35	Asn Thr Gly Gln Ile Asp Asp Pro Gln Glu Gln His Arg Val Ile Ser	

128/177

	130	135	140	
	agc aac ctg gcc ctc atc cag gtg cag gcc act gtc gtg ggg ctc ttg			535
	Ser Asn Leu Ala Leu Ile Gln Val Gln Ala Thr Val Val Gly Leu Leu			
	145	150	155	160
5	gct gct gtg gct gcg ctg ctg ttg ggc gtg gtg tct cga gag gaa gtg			583
	Ala Ala Val Ala Ala Leu Leu Leu Gly Val Val Ser Arg Glu Glu Val			
	165	170	175	
	gat gtc gcc aag gtg gag ttg ctg tgt gcc agc agt gtc ctc act gcc			631
	Asp Val Ala Lys Val Glu Leu Leu Cys Ala Ser Ser Val Leu Thr Ala			
10	180	185	190	
	ttc ctt gca gcc ttt gcc ctg ggg gtg ctg atg gtc tgt ata gtg att			679
	Phe Leu Ala Ala Phe Ala Leu Gly Val Leu Met Val Cys Ile Val Ile			
	195	200	205	
	ggg gct cga aag ctc ggg gtc aac cca gac aac att gcc acg ccc att			727
15	Gly Ala Arg Lys Leu Gly Val Asn Pro Asp Asn Ile Ala Thr Pro Ile			
	210	215	220	
	gca gcc agc ctg gga gac ctc atc aca ctg tcc att ctg gct ttg gtt			775
	Ala Ala Ser Leu Gly Asp Leu Ile Thr Leu Ser Ile Leu Ala Leu Val			
	225	230	235	240
20	agc agc ttc ttc tac aga cac aaa gat agt cgg tat ctg acg ccg ctg			823
	Ser Ser Phe Phe Tyr Arg His Lys Asp Ser Arg Tyr Leu Thr Pro Leu			
	245	250	255	
	gtc tgc ctc agc ttt gcg gct ctg acc cca gtg tgg gtc ctc att gcc			871
	Val Cys Leu Ser Phe Ala Ala Leu Thr Pro Val Trp Val Leu Ile Ala			
25	260	265	270	
	aag cag agc cca ccc atc gtg aag atc ctg aag ttt ggc tgg ttc cca			919
	Lys Gln Ser Pro Pro Ile Val Lys Ile Leu Lys Phe Gly Trp Phe Pro			
	275	280	285	
	atc atc ctg gcc atg gtc atc agc agt ttc gga gga ctc atc ttg agc			967
30	Ile Ile Leu Ala Met Val Ile Ser Ser Phe Gly Gly Leu Ile Leu Ser			
	290	295	300	
	aaa acc gtt tct aaa cag cag tac aaa ggc atg gcg ata ttt acc ccc			1015
	Lys Thr Val Ser Lys Gln Gln Tyr Lys Gly Met Ala Ile Phe Thr Pro			
	305	310	315	320
35	gtc ata tgt ggt gtt ggt ggc aat ctg gtg gcc att cag acc agc cga			1063

129/177

	Val Ile Cys Gly Val Gly Gly Asn Leu Val Ala Ile Gln Thr Ser Arg	
	325 330 335	
	atc tca acc tac ctg cac atg tgg agt gca cct ggc gtc ctg ccc etc	1111
	Ile Ser Thr Tyr Leu His Met Trp Ser Ala Pro Gly Val Leu Pro Leu	
5	340 345 350	
	cag atg aag aaa ttc tgg ccc aac ccg tgt tct act ttc tgc acg tca	1159
	Gln Met Lys Lys Phe Trp Pro Asn Pro Cys Ser Thr Phe Cys Thr Ser	
	355 360 365	
	gaa atc aat tcc atg tca gct cga gtc ctg ctc ttg ctg gtg gtc cca	1207
10	Glu Ile Asn Ser Met Ser Ala Arg Val Leu Leu Leu Leu Val Val Pro	
	370 375 380	
	ggc cat ctg att ttc ttc tac atc atc tac ctg gtg gag ggt cag tca	1255
	Gly His Leu Ile Phe Phe Tyr Ile Ile Tyr Leu Val Glu Gly Gln Ser	
	385 390 395 400	
15	gtc ata aac agc cag acc ttt gtg gtg ctc tac ctg ctg gca ggc ctg	1303
	Val Ile Asn Ser Gln Thr Phe Val Val Leu Tyr Leu Leu Ala Gly Leu	
	405 410 415	
	atc cag gtg aca atc ctg ctg tac ctg gca gaa gtg atg gtt cgg ctg	1351
	Ile Gln Val Thr Ile Leu Leu Tyr Leu Ala Glu Val Met Val Arg Leu	
20	420 425 430	
	act tgg cac cag gcc ctg gat cct gac aac cac tgc atc ccc tac ctt	1399
	Thr Trp His Gln Ala Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu	
	435 440 445	
	aca ggg ctg ggg gac ctg ctc ggt act ggc ctc ctg gca ctc tgc ttt	1447
25	Thr Gly Leu Gly Asp Leu Leu Gly Thr Gly Leu Leu Ala Leu Cys Phe	
	450 455 460	
	ttc act gac tgg cta ctg aag agc aag gca gag ctg ggt ggc atc tca	1495
	Phe Thr Asp Trp Leu Leu Lys Ser Lys Ala Glu Leu Gly Gly Ile Ser	
	465 470 475 480	
30	gaa ctg gca tct gga cct ccc taactgggcc ccgctggtcc catttgctca ttag	1550
	Glu Leu Ala Ser Gly Pro Pro	
	485	
	aatttctct cacaatcagt ggatacagaa ttcagtttct cccttgccag gtccttgga	1610
	tgggtgaccc ctgcctctgc agtagccttt tgtgagctctg ctaaggtagc tctcacacac	1670
35	ctcggtctctg ggggtgatac ctgagcctgc aatagagccc tgaaatcaag agcatggctt	1730

130/177

	gagtgtgtga atatgatgtg tgcacatgct taatgagcgt gcaagtgtgc acacgtttgt	1790
	ggagaggagg gtgttctggc ctgagaagct aaagaagagg catgtccagt atgctttgca	1850
	gggtgtgttt gctctttttcc atgcccacgc aaccacagatt ggggtggagc aggaaggagc	1910
	tcttttctgt tcccaagcct cagaactcct gagctgtggc ttacttgctg tcttcaccag	1970
5	gttcaagctc cgtggggccac actgctgctg tgccaagaag gtgtacagcc tccccaggat	2030
	ggggcctcat acaacccttc atctgcactc aacatttaac cgtgtccttg ctgtcttttt	2090
	attttccttt ttgttagcaa aaacctctat ttagatttca ataatacagag aagtgtaaaa	2150
	taaaacagat tatattgt	2168
10	<210> 116	
	<211> 1357	
	<212> DNA	
	<213> Homo Sapiens	
	<220>	
15	<221> CDS	
	<222> (81)...(1262)	
	<400> 116	
	cgtgcgtttg tggecgtecg geeteectga catgcagecc tctggacccc gaggttggac	60
20	cctactgtga cacacctacc atg cgg aca ctc ttc aac ctc ctc tgg ctt	110
	Met Arg Thr Leu Phe Asn Leu Leu Trp Leu	
	1 5 10	
	gcc ctg gcc tgc agc cct gtt cac act acc ctg tca aag tca gat gcc	158
	Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala	
25	15 20 25	
	aaa aaa gcc gcc tca aag acg ctg ctg gag aag agt cag ttt tca gat	203
	Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp	
	30 35 40	
	aag ccg gtg caa gac cgg ggt ttg gtg gtg acg gac ctc aaa gct gag	254
30	Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu	
	45 50 55	
	agt gtg gtt ctt gag cat cgc agc tac tgc tcg gca aag gcc cgg gac	302
	Ser Val Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp	
	60 65 70	
35	aga cac ttt gct ggg gat gta ctg ggc tat gtc act cca tgg aac agc	350

131/177

	Arg His Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser	
	75	80 85 90
	cat ggc tac gat gtc acc aag gtc ttt ggg agc aag ttc aca cag atc	398
5	His Gly Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile	
	95 100 105	
	tca ccc gtc tgg ctg cag ctg aag aga cgt ggc cgt gag atg ttt gag	446
	Ser Pro Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu	
	110 115 120	
10	gtc acg ggc ctc cac gac gtg gac caa ggg tgg atg cga gct gtc agg	494
	Val Thr Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg	
	125 130 135	
	aag cat gcc aag ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac	542
	Lys His Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp	
	140 145 150	
15	tgg act tac gat gat ttc cgg aac gtc tta gac agt gag gat gag ata	590
	Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile	
	155 160 165 170	
	gag gag ctg agc aag acc gtg gtc cag gtg gca aag aac cag cat ttc	638
	Glu Glu Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe	
20	175 180 185	
	gat ggc ttc gtg gtg gag gtc tgg aac cag ctg cta agc cag aag cgc	686
	Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg	
	190 195 200	
25	gtg ggc ctc atc cac atg ctc acc cac ttg gcc gag gct ctg cac cag	734
	Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln	
	205 210 215	
	gcc cgg ctg ctg gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg	782
	Ala Arg Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly	
	220 225 230	
30	acc gac cag ctg ggc atg ttc acg cac aag gag ttt gag cag ctg gcc	830
	Thr Asp Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala	
	235 240 245 250	
	ccc gtg ctg gat ggt ttc agc ctc atg acc tac gac tac tct aca gcg	878
	Pro Val Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala	
35	255 260 265	

132/177

cat cag cct ggc cct aat gca ccc ctg tcc tgg gtt cga gcc tgc gtc 926
 His Gln Pro Gly Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val
 270 275 280
 cag gtc ctg gac ccg aag tcc aag tgg cga agc aaa atc ctc ctg ggg 974
 5 Gln Val Leu Asp Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly
 285 290 295
 ctc aac ttc tat ggt atg gac tac gcg acc tcc aag gat gcc cgt gag 1022
 Leu Asn Phe Tyr Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu
 300 305 310
 cct gtt gtc ggg gcc agg tac atc cag aca ctg aag gac cac agg ccc 1070
 10 Pro Val Val Gly Ala Arg Tyr Ile Gln Thr Leu Lys Asp His Arg Pro
 315 320 325 330
 cgg atg gtg tgg gac agc cag gcc tca gag cac ttc ttc gag tac aag 1118
 Arg Met Val Trp Asp Ser Gln Ala Ser Glu His Phe Phe Glu Tyr Lys
 15 335 340 345
 aag agc cgc agt ggg agg cac gtc gtc ttc tac cca acc ctg aag tcc 1166
 Lys Ser Arg Ser Gly Arg His Val Val Phe Tyr Pro Thr Leu Lys Ser
 350 355 360
 ctg cag gtg cgg ctg gag ctg gcc cgg gag ctg ggc gtt ggg gtc tct 1214
 20 Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly Val Gly Val Ser
 365 370 375
 atc tgg gag ctg ggc cag gcc ctg gac tac ttc tac gac ctg ctc t 1260
 Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu
 380 385 390
 aggtgggcat tgcggcctcc gcggtggacg tgttcttttc taagccatgg agtgagtgag 1320
 25 caggtgtgaa atacaggcct ccactccgtt tgctgtg 1357

<210> 117

<211> 711

30 <212> DNA

<213> Homo Sapience

<220>

<221> CDS

<222> (8)...(598)

35

133/177

<400> 117

	aaaggcg atg tgg agg gtg ccc ggc aca acc aga cgc cca gtc aca ggc	49
	Met Trp Arg Val Pro Gly Thr Thr Arg Arg Pro Val Thr Gly	
	1 5 10	
5	gag agc cct ggg atg cac cgg cca gag gcc atg ctg ctg ctg ctc acg	97
	Glu Ser Pro Gly Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr	
	15 20 25 30	
	ctt gcc ctc ctg ggg ggc ccc acc tgg gca ggg aag atg tat ggc cct	145
	Leu Ala Leu Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro	
10	35 40 45	
	gga gga ggc aag tat ttc agc acc act gaa gac tac gac cat gaa atc	193
	Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile	
	50 55 60	
	aca ggg ctg cgg gtg tct gta ggt ctt ctc ctg gtg aaa agt gtc cag	241
15	Thr Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln	
	65 70 75	
	gtg aaa ctt gga gac tcc tgg gac gtg aaa ctg gga gcc tta ggt ggg	289
	Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly Gly	
	80 85 90	
20	aat acc cag gaa gtc acc ctg cag cca ggc gaa tac atc aca aaa gtc	337
	Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr Lys Val	
	95 100 105 110	
	ttt gtc gcc ttc caa gct ttc ctc cgg ggt atg gtc atg tac acc agc	385
	Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met Tyr Thr Ser	
25	115 120 125	
	aag gac cgc tat ttc tat ttt ggg aag ctt gat ggc cag atc tcc tct	433
	Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly Gln Ile Ser Ser	
	130 135 140	
	gcc tac ccc agc caa gag ggg cag gtg ctg gtg ggc atc tat ggc cag	481
30	Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val Gly Ile Tyr Gly Gln	
	145 150 155	
	tat caa ctc ctt ggc atc aag agc att ggc ttt gaa tgg aat tat cca	529
	Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly Phe Glu Trp Asn Tyr Pro	
	160 165 170	
35	cta gag gag ccg acc act gag cca cca gtt aat ctc aca tac tca gca	577

134/177

Leu Glu Glu Pro Thr Thr Glu Pro Pro Val Asn Leu Thr Tyr Ser Ala
 175 180 185 190
 aac tca ccc gtg ggt cgc taggggtggg tatggggcca tccgagctga ggcca 630
 Asn Ser Pro Val Gly Arg
 5 195
 tctgtgtggt ggtggctgat ggtactggag taactgagtc gggacgctga atctgaatcc 690
 accaataaat aaagcttctg c 711

 <210> 118
 10 <211> 651
 <212> DNA
 <213> Homo Sapience
 <220>
 <221> CDS
 15 <222> (242)...(565)

 <400> 118
 aaagaaacaa gccgggggac tgcgagccag ggactcgggc cgcggggcgga gaagaagtgg 60
 ggcagcgtt ggccaggccg aaaggacttt gggggtggg gctgggagtc cgtgtctcga 120
 20 atgagggagg agaggtggag ttgccggggc tcaggcccg cctcgagcat gggcggatga 180
 gaggagtcgg gagccgaggc ctagggtcct tcgggtgagg ggagacggag ccagcgagga 240
 g atg gag cag aag ctt gtg gag gag att ctt caa gca atc act atg 286
 Met Glu Gln Lys Leu Val Glu Glu Ile Leu Gln Ala Ile Thr Met
 1 5 10 15
 25 tca aca gac aca ggt gtt tcc ctt cct tca tat gag gaa gat cag gga 334
 Ser Thr Asp Thr Gly Val Ser Leu Pro Ser Tyr Glu Glu Asp Gln Gly
 20 25 30
 tca aaa ctc att cga aaa gct aaa gag gca cca ttc gta ccc gtt gga 382
 Ser Lys Leu Ile Arg Lys Ala Lys Glu Ala Pro Phe Val Pro Val Gly
 30 35 40 45
 ata gcg ggt ttt gca gca att gtt gca tat gga tta tat aaa ctg aag 430
 Ile Ala Gly Phe Ala Ala Ile Val Ala Tyr Gly Leu Tyr Lys Leu Lys
 50 55 60
 agc agg gga aat act aaa atg tcc att cat ctg atc cac atg cgt gtg 478
 35 Ser Arg Gly Asn Thr Lys Met Ser Ile His Leu Ile His Met Arg Val

135/177

	65	70	75	
	gca gcc caa ggc ttt gtt gta gga gca atg act gtt ggt atg ggc tat			526
	Ala Ala Gln Gly Phe Val Val Gly Ala Met Thr Val Gly Met Gly Tyr			
	80	85	90	95
5	tcc atg tat cgg gaa ttc tgg gca aaa cct aag cct tagaagaa			570
	Ser Met Tyr Arg Glu Phe Trp Ala Lys Pro Lys Pro			
	100	105		
	gagatgctgt cttggtcttg ttggaggagc ttgctttagt tagatgtctt attattaaag			630
	ttacctatta ttgttggaat			651
10				
	<210> 119			
	<211> 1310			
	<212> DNA			
	<213> Homo Sapience			
15	<220>			
	<221> CDS			
	<222> (78)...(1130)			
	<400> 119			
20	cgaacgccaa ggcggccacg tctgctccc cctggtgaag aagctgccct gggcttgctg			60
	tctagggtc tccagac atg tct gag gtg aag agc cgg aag aag tcg ggg			110
	Met Ser Glu Val Lys Ser Arg Lys Lys Ser Gly			
	1	5	10	
	ccc aag gga gcc cct gct gcg gag ccc ggg aag cgg agc gag ggc ggg			158
25	Pro Lys Gly Ala Pro Ala Ala Glu Pro Gly Lys Arg Ser Glu Gly Gly			
	15	20	25	
	aag acc ccc gtg gcc cgg agc agc gga ggc ggg ggc tgg gca gac ccc			206
	Lys Thr Pro Val Ala Arg Ser Ser Gly Gly Gly Gly Trp Ala Asp Pro			
	30	35	40	
30	cga acg tgc ctg agc ctg ctg tcg ctg ggg acg tgc ctg ggc ctg gcc			254
	Arg Thr Cys Leu Ser Leu Leu Ser Leu Gly Thr Cys Leu Gly Leu Ala			
	45	50	55	
	tgg ttt gta ttt cag cag tca gaa aaa ttt gca aag gtg gaa aac caa			302
	Trp Phe Val Phe Gln Gln Ser Glu Lys Phe Ala Lys Val Glu Asn Gln			
35	60	65	70	75

136/177

	tac cag tta ctg aaa cta gaa acc aat gaa ttc caa caa ctt caa agt	350
	Tyr Gln Leu Leu Lys Leu Glu Thr Asn Glu Phe Gln Gln Leu Gln Ser	
	80 85 90	
	aaa atc agt tta att tca gaa aag tgg cag aaa tct gaa gct atc atg	398
5	Lys Ile Ser Leu Ile Ser Glu Lys Trp Gln Lys Ser Glu Ala Ile Met	
	95 100 105	
	gaa caa ttg aag tct ttt caa ata att gct cat cta aag cgt cta cag	446
	Glu Gln Leu Lys Ser Phe Gln Ile Ile Ala His Leu Lys Arg Leu Gln	
	110 115 120	
10	gaa gaa att aat gag gta aaa act tgg tcc aat agg ata act gaa aaa	494
	Glu Glu Ile Asn Glu Val Lys Thr Trp Ser Asn Arg Ile Thr Glu Lys	
	125 130 135	
	cag gat ata ctg aac aac agt ctg acg acg ctt tct caa gac att aca	542
	Gln Asp Ile Leu Asn Asn Ser Leu Thr Thr Leu Ser Gln Asp Ile Thr	
15	140 145 150 155	
	aaa gta gac caa agt aca act tcc atg gca aaa gat gtt ggt ctc aag	590
	Lys Val Asp Gln Ser Thr Thr Ser Met Ala Lys Asp Val Gly Leu Lys	
	160 165 170	
	att aca agt gta aaa aca gat ata cga cgg att tca ggt tta gta act	638
20	Ile Thr Ser Val Lys Thr Asp Ile Arg Arg Ile Ser Gly Leu Val Thr	
	175 180 185	
	gat gta ata tca ttg aca gat tct gtg caa gaa cta gaa aat aaa ata	686
	Asp Val Ile Ser Leu Thr Asp Ser Val Gln Glu Leu Glu Asn Lys Ile	
	190 195 200	
25	gag aaa gta gaa aaa aat aca gta aaa aat ata ggt gat ctt ctt tca	734
	Glu Lys Val Glu Lys Asn Thr Val Lys Asn Ile Gly Asp Leu Leu Ser	
	205 210 215	
	agc agt att gat cga aca gca acg ctc cga aag aca gca tct gaa aat	782
	Ser Ser Ile Asp Arg Thr Ala Thr Leu Arg Lys Thr Ala Ser Glu Asn	
30	220 225 230 235	
	tca caa aga att aac tct gtt aag aag acg cta acc gaa cta aag agt	830
	Ser Gln Arg Ile Asn Ser Val Lys Lys Thr Leu Thr Glu Leu Lys Ser	
	240 245 250	
	gac ttc gac aaa cat aca gat aga ttt cta agc tta gaa ggt gac aga	878
35	Asp Phe Asp Lys His Thr Asp Arg Phe Leu Ser Leu Glu Gly Asp Arg	

137/177

	255	260	265	
	gcc aaa gtt ctg aag aca gtg act ttt gca aat gat cta aaa cca aag			926
	Ala Lys Val Leu Lys Thr Val Thr Phe Ala Asn Asp Leu Lys Pro Lys			
	270	275	280	
5	gtg tat aat cta aag aag gac ttt tcc cgt tta gaa cca tta gta aat			974
	Val Tyr Asn Leu Lys Lys Asp Phe Ser Arg Leu Glu Pro Leu Val Asn			
	285	290	295	
	gat tta aca cta cgc att ggg aga ttg gtt acc gac tta cta caa aga			1022
	Asp Leu Thr Leu Arg Ile Gly Arg Leu Val Thr Asp Leu Leu Gln Arg			
10	300	305	310	315
	gag aaa gaa att gct ttc tta agt gaa aaa ata tct aat tta aca ata			1070
	Glu Lys Glu Ile Ala Phe Leu Ser Glu Lys Ile Ser Asn Leu Thr Ile			
	320	325	330	
	gtc caa gct gag att aag gat att aaa gat gaa ata gca cac att tca			1118
15	Val Gln Ala Glu Ile Lys Asp Ile Lys Asp Glu Ile Ala His Ile Ser			
	335	340	345	
	gat atg aat tagtttgaca ttattgagat tagactaagg taattttttt aat			1170
	Asp Met Asn			
	350			
20	gggacctctc atgagaagac tggtaaataca aaaataatga tattttggag caaaagtcac			1230
	tttatattta atcctatattt gtacagtaaa aataaaaactt taaaacaggt tgattttcca			1290
	aaataaatat gctaaaacct			1310
	<210> 120			
25	<211> 1400			
	<212> DNA			
	<213> Homo Sapience			
	<220>			
	<221> CDS			
30	<222> (233)...(556)			
	<400> 120			
	tggtctgatg ctattggagg gtggaaatca catctoctgt ttatccgtgt gcttgtagg			60
	tgtcagccgc ccccccccc ccatatgcag atttactcgg catggtagtg gccagcttct			120
35	aacacagctg gtatttcaag tctcctggga cctcactcag gaatgatacc cctcagtag			180

138/177

	aagcagcagg tgatcttaac tcctttcaaaa gagcaggcct gtctgggaag cc atg	235
	Met	
	1	
	tcc tca gca ggc aca gca acc cct ctg gaa atg gat cac aaa ctc act	283
5	Ser Ser Ala Gly Thr Ala Thr Pro Leu Glu Met Asp His Lys Leu Thr	
	5 10 15	
	tct cag cca ggc agg cca agc ttc tat tgt aac agt agg cac agt ata	331
	Ser Gln Pro Gly Arg Pro Ser Phe Tyr Cys Asn Ser Arg His Ser Ile	
	20 25 30	
10	gtc gga tca tca cat cag ctg ggt ttt tgg ttt agt cat cta gag tcg	379
	Val Gly Ser Ser His Gln Leu Gly Phe Trp Phe Ser His Leu Glu Ser	
	35 40 45	
	tct gga cta aag gtc ttt cag gtc tcc ttg ccc tgt gag tgc gtg aac	427
	Ser Gly Leu Lys Val Phe Gln Val Ser Leu Pro Cys Glu Cys Val Asn	
15	50 55 60 65	
	ctc ccc acc cga att gcc tca gtt gtc ctg agc ctc atg tot ctc ctg	475
	Leu Pro Thr Arg Ile Ala Ser Val Val Leu Ser Leu Met Ser Leu Leu	
	70 75 80	
	gtg gtg ggc cag gcc cct gca tgg gaa ggg agc ctg ctg cgg ggc agg	523
20	Val Val Gly Gln Ala Pro Ala Trp Glu Gly Ser Leu Leu Arg Gly Arg	
	85 90 95	
	cca gct ggg ggt gct cac cta tgc gca gca tgaagttatt gaaggac	570
	Pro Ala Gly Gly Ala His Leu Cys Ala Ala	
	100 105	
25	tggttggtga tggtggtgag cgtatccttc atggccagcg cgaagtcggc caggtcagcc	630
	aggtgctgcc agcgtctct ctcggacttg tcttcctgtg ccaggggacc gtggagaaag	690
	tgtcaggggc cgtcactgc agcagcctgc tctgtgcct tccttggcag tggtctgggg	750
	gtggattccc tacacctaga tggtcaaggc cttacttttc ctcccacaaa ggagtcgcag	810
	ccacgctagc tctgacttgc cactgtgaca aagttcacgt agcaggtcta ggcaaagact	870
30	gggcaattga gcagaggaga cggacctgtg agtctgacca cgaggcggac cccttcacct	930
	tggtctggcc tggtcctggt ccttaggttt tgtcagggtg tccttggttg gatccctcaa	990
	ctaggtgata agcactggag ggggatgacc cgccttgac gtgtttcttt aacctcatcc	1050
	atataatagg gccgtgggat gggtgtagag gtaaagcagg atgatggtgt ttttaagacca	1110
	gagcttgga ccagggctcc tacacctaat tttctctcct ggtagctgaa caaaggtcta	1170
35	aattagctta acaaaagaac aggctgccgt cagccagagt tctgaaggcc atgctttcag	1230

139/177

tttcccttgt tgacaattgc tctccagttc ctatgaaagc acagagcctt aggggggcctg 1290
gccacagaac acaaccatct taggcctgag ctgtgaacag caggggggttg tgtgtctgtt 1350
ctgtttctct gcttgccgaa cttttctcaat aaaccctatt tcttatttat 1400

5 <210> 121
<211> 483
<212> PRT
<213> Homo sapience

10 <400> 121
Met Lys Ala Phe His Thr Phe Cys Val Val Leu Leu Val Phe Gly Ser
1 5 10 15
Val Ser Glu Ala Lys Phe Asp Asp Phe Glu Asp Glu Glu Asp Ile Val
20 25 30
15 Glu Tyr Asp Asp Asn Asp Phe Ala Glu Phe Glu Asp Val Met Glu Asp
35 40 45
Ser Val Thr Glu Ser Pro Gln Arg Val Ile Ile Thr Glu Asp Asp Glu
50 55 60
Asp Glu Thr Thr Val Glu Leu Glu Gly Gln Asp Glu Asn Gln Glu Gly
20 65 70 75 80
Asp Phe Glu Asp Ala Asp Thr Gln Glu Gly Asp Thr Glu Ser Glu Pro
85 90 95
Tyr Asp Asp Glu Glu Phe Glu Gly Tyr Glu Asp Lys Pro Asp Thr Ser
100 105 110
25 Ser Ser Lys Asn Lys Asp Pro Ile Thr Ile Val Asp Val Pro Ala His
115 120 125
Leu Gln Asn Ser Trp Glu Ser Tyr Tyr Leu Glu Ile Leu Met Val Thr
130 135 140
Gly Leu Leu Ala Tyr Ile Met Asn Tyr Ile Ile Gly Lys Asn Lys Asn
30 145 150 155 160
Ser Arg Leu Ala Gln Ala Trp Phe Asn Thr His Arg Glu Leu Leu Glu
165 170 175
Ser Asn Phe Thr Leu Val Gly Asp Asp Gly Thr Asn Lys Glu Ala Thr
180 185 190
35 Ser Thr Gly Lys Leu Asn Gln Glu Asn Glu His Ile Tyr Asn Leu Trp

140/177

	195	200	205
	Cys Ser Gly Arg Val Cys Cys Glu Gly Met Leu Ile Gln Leu Arg Phe		
	210	215	220
5	Leu Lys Arg Gln Asp Leu Leu Asn Val Leu Ala Arg Met Met Arg Pro		
	225	230	235
	Val Ser Asp Gln Val Gln Ile Lys Val Thr Met Asn Asp Glu Asp Met		
	245	250	255
	Asp Thr Tyr Val Phe Ala Val Gly Thr Arg Lys Ala Leu Val Arg Leu		
	260	265	270
10	Gln Lys Glu Met Gln Asp Leu Ser Glu Phe Cys Ser Asp Lys Pro Lys		
	275	280	285
	Ser Gly Ala Lys Tyr Gly Leu Pro Asp Ser Leu Ala Ile Leu Ser Glu		
	290	295	300
	Met Gly Glu Val Thr Asp Gly Met Met Asp Thr Lys Met Val His Phe		
15	305	310	315
	Leu Thr His Tyr Ala Asp Lys Ile Glu Ser Val His Phe Ser Asp Gln		
	325	330	335
	Phe Ser Gly Pro Lys Ile Met Gln Glu Glu Gly Gln Pro Leu Lys Leu		
	340	345	350
20	Pro Asp Thr Lys Arg Thr Leu Leu Phe Thr Phe Asn Val Pro Gly Ser		
	355	360	365
	Gly Asn Thr Tyr Pro Lys Asp Met Glu Ala Leu Leu Pro Leu Met Asn		
	370	375	380
	Met Val Ile Tyr Ser Ile Asp Lys Ala Lys Lys Phe Arg Leu Asn Arg		
25	385	390	395
	Glu Gly Lys Gln Lys Ala Asp Lys Asn Arg Ala Arg Val Glu Glu Asn		
	405	410	415
	Phe Leu Lys Leu Thr His Val Gln Arg Gln Glu Ala Ala Gln Ser Arg		
	420	425	430
30	Arg Glu Glu Lys Lys Arg Ala Glu Lys Glu Arg Ile Met Asn Glu Glu		
	435	440	445
	Asp Pro Glu Lys Gln Arg Arg Leu Glu Glu Ala Ala Leu Arg Arg Glu		
	450	455	460
	Gln Lys Lys Leu Glu Lys Lys Gln Met Lys Met Lys Gln Ile Lys Val		
35	465	470	475
			480

141/177

Lys Ala Met

<210> 122

<211> 334

5 <212> PRT

<213> Homo sapience

<400> 122

Met Val Glu Phe Ala Pro Leu Phe Met Pro Trp Glu Arg Arg Leu Gln
 10 1 5 10 15
 Thr Leu Ala Val Leu Gln Phe Val Phe Ser Phe Leu Ala Leu Ala Glu
 20 25 30
 Ile Cys Thr Val Gly Phe Ile Ala Leu Leu Phe Thr Arg Phe Trp Leu
 35 40 45
 15 Leu Thr Val Leu Tyr Ala Ala Trp Trp Tyr Leu Asp Arg Asp Lys Pro
 50 55 60
 Arg Gln Gly Gly Arg His Ile Gln Ala Ile Arg Cys Trp Thr Ile Trp
 65 70 75 80
 Lys Tyr Met Lys Asp Tyr Phe Pro Ile Ser Leu Val Lys Thr Ala Glu
 20 85 90 95
 Leu Asp Pro Ser Arg Asn Tyr Ile Ala Gly Phe His Pro His Gly Val
 100 105 110
 Leu Ala Val Gly Ala Phe Ala Asn Leu Cys Thr Glu Ser Thr Gly Phe
 115 120 125
 25 Ser Ser Ile Phe Pro Gly Ile Arg Pro His Leu Met Met Leu Thr Leu
 130 135 140
 Trp Phe Arg Ala Pro Phe Phe Arg Asp Tyr Ile Met Ser Ala Gly Leu
 145 150 155 160
 Val Thr Ser Glu Lys Glu Ser Ala Ala His Ile Leu Asn Arg Lys Gly
 30 165 170 175
 Gly Gly Asn Leu Leu Gly Ile Ile Val Gly Gly Ala Gln Glu Ala Leu
 180 185 190
 Asp Ala Arg Pro Gly Ser Phe Thr Leu Leu Leu Arg Asn Arg Lys Gly
 195 200 205
 35 Phe Val Arg Leu Ala Leu Thr His Gly Ala Pro Leu Val Pro Ile Phe

142/177

210 215 220
 Ser Phe Gly Glu Asn Asp Leu Phe Asp Gln Ile Pro Asn Ser Ser Gly
 225 230 235 240
 Ser Trp Leu Arg Tyr Ile Gln Asn Arg Leu Gln Lys Ile Met Gly Ile
 5 245 250 255
 Ser Leu Pro Leu Phe His Gly Arg Gly Val Phe Gln Tyr Ser Phe Gly
 260 265 270
 Leu Ile Pro Tyr Arg Arg Pro Ile Thr Thr Val Val Gly Lys Pro Ile
 275 280 285
 10 Glu Val Gln Lys Thr Leu His Pro Ser Glu Glu Glu Val Asn Gln Leu
 290 295 300
 His Gln Arg Tyr Ile Lys Glu Leu Cys Asn Leu Phe Glu Ala His Lys
 305 310 315 320
 Leu Lys Phe Asn Ile Pro Ala Asp Gln His Leu Glu Phe Cys
 15 325 330

 <210> 123
 <211> 267
 <212> PRT
 20 <213> Homo sapience

 <400> 123
 Met Ala Pro Trp Ala Leu Leu Ser Pro Gly Val Leu Val Arg Thr Gly
 1 5 10 15
 25 His Thr Val Leu Thr Trp Gly Ile Thr Leu Val Leu Phe Leu His Asp
 20 25 30
 Thr Glu Leu Arg Gln Trp Glu Glu Gln Gly Glu Leu Leu Leu Pro Leu
 35 40 45
 Thr Phe Leu Leu Leu Val Leu Gly Ser Leu Leu Leu Tyr Leu Ala Val
 30 50 55 60
 Ser Leu Met Asp Pro Gly Tyr Val Asn Val Gln Pro Gln Pro Gln Glu
 65 70 75 80
 Glu Leu Lys Glu Glu Gln Thr Ala Met Val Pro Pro Ala Ile Pro Leu
 85 90 95
 35 Arg Arg Cys Arg Tyr Cys Leu Val Leu Gln Pro Leu Arg Ala Arg His

143/177

100 105 110
 Cys Arg Glu Cys Arg Arg Cys Val Arg Arg Tyr Asp His His Cys Pro
 115 120 125
 Trp Met Glu Asn Cys Val Gly Glu Arg Asn His Pro Leu Phe Val Val
 5 130 135 140
 Tyr Leu Ala Leu Gln Leu Val Val Leu Leu Trp Gly Leu Tyr Leu Ala
 145 150 155 160
 Trp Ser Gly Leu Arg Phe Phe Gln Pro Trp Gly Leu Trp Leu Arg Ser
 165 170 175
 10 Ser Gly Leu Leu Phe Ala Thr Phe Leu Leu Leu Ser Leu Phe Ser Leu
 180 185 190
 Val Ala Ser Leu Leu Leu Val Ser His Leu Tyr Leu Val Ala Ser Asn
 195 200 205
 Thr Thr Thr Trp Glu Phe Ile Ser Ser His Arg Ile Ala Tyr Leu Arg
 15 210 215 220
 Gln Arg Pro Ser Asn Pro Phe Asp Arg Gly Leu Thr Arg Asn Leu Ala
 225 230 235 240
 His Phe Phe Cys Gly Trp Pro Ser Gly Ser Trp Glu Thr Leu Trp Ala
 245 250 255
 20 Glu Glu Glu Glu Glu Gly Ser Ser Pro Ala Val
 260 265

 <210> 124
 <211> 106
 25 <212> PRT
 <213> Homo sapience

 <400> 124
 Met Ser Thr Asn Asn Met Ser Asp Pro Arg Arg Pro Asn Lys Val Leu
 30 1 5 10 15
 Arg Tyr Lys Pro Pro Pro Ser Glu Cys Asn Pro Ala Leu Asp Asp Pro
 20 25 30
 Thr Pro Asp Tyr Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly
 35 35 40 45
 Leu Met Leu Lys Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser

144/177

50 55 60
 Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met
 65 70 75 80
 Met Ser Ser Phe Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu
 5 85 90 95
 Gln Asn Pro Gln Pro Met Thr Pro Pro Trp
 100 105

 <210> 125
 10 <211> 224
 <212> PRT
 <213> Homo sapience

 <400> 125
 15 Met Thr Leu Phe His Phe Gly Asn Cys Phe Ala Leu Ala Tyr Phe Pro
 1 5 10 15
 Tyr Phe Ile Thr Tyr Lys Cys Ser Gly Leu Ser Glu Tyr Asn Ala Phe
 20 20 25 30
 Trp Lys Cys Val Gln Ala Gly Val Thr Tyr Leu Phe Val Gln Leu Cys
 20 35 40 45
 Lys Met Leu Phe Leu Ala Thr Phe Phe Pro Thr Trp Glu Gly Gly Ile
 50 55 60
 Tyr Asp Phe Ile Gly Glu Phe Met Lys Ala Ser Val Asp Val Ala Asp
 65 70 75 80
 25 Leu Ile Gly Leu Asn Leu Val Met Ser Arg Asn Ala Gly Lys Gly Glu
 85 90 95
 Tyr Lys Ile Met Val Ala Ala Leu Gly Trp Ala Thr Ala Glu Leu Ile
 100 105 110
 Met Ser Arg Cys Ile Pro Leu Trp Val Gly Ala Arg Gly Ile Glu Phe
 30 115 120 125
 Asp Trp Lys Tyr Ile Gln Met Ser Ile Asp Ser Asn Ile Ser Leu Val
 130 135 140
 His Tyr Ile Val Ala Ser Ala Gln Val Trp Met Ile Thr Arg Tyr Asp
 145 150 155 160
 35 Leu Tyr His Thr Phe Arg Pro Ala Val Leu Leu Leu Met Phe Leu Ser

145/177

165 170 175
 Val Tyr Lys Ala Phe Val Met Glu Thr Phe Val His Leu Cys Ser Leu
 180 185 190
 Gly Ser Trp Ala Ala Leu Leu Ala Arg Ala Val Val Thr Gly Leu Leu
 5 195 200 205
 Ala Leu Ser Thr Leu Ala Leu Tyr Val Ala Val Val Asn Val His Ser
 210 215 220

 <210> 126
 10 <211> 258
 <212> PRT
 <213> Homo sapience

 <400> 126
 15 Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
 1 5 10 15
 Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
 20 20 25 30
 Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
 20 35 40 45
 Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
 50 55 60
 Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
 65 70 75 80
 25 Arg Arg Ser Met Phe Leu Met Thr Cys Lys Pro Pro Leu Tyr Met Gly
 85 90 95
 Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys Thr Ile Asp Glu Glu Leu
 100 105 110
 Glu Arg Asp Lys Arg Val Thr Trp Ile Val Glu Phe Phe Ala Asn Trp
 30 115 120 125
 Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile Tyr Ala Asp Leu Ser Leu
 130 135 140
 Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly Lys Val Asp Val Gly Arg
 145 150 155 160
 35 Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val Ser Thr Ser Pro Leu Thr

146/177

165 170 175
 Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln Gly Gly Lys Glu Ala Met
 180 185 190
 Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg Ala Val Ser Trp Thr Phe
 5 195 200 205
 Ser Glu Glu Asn Val Ile Arg Glu Phe Asn Leu Asn Glu Leu Tyr Gln
 210 215 220
 Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp Asn Ile Pro Glu Glu Gln
 225 230 235 240
 10 Pro Val Ala Ser Thr Pro Thr Thr Val Ser Asp Gly Glu Asn Lys Lys
 245 250 255
 Asp Lys

 <210> 127
 15 <211> 110
 <212> PRT
 <213> Homo sapience

 <400> 127
 20 Met Ala Ala Val Val Ala Lys Arg Glu Gly Pro Pro Phe Ile Ser Glu
 1 5 10 15
 Ala Ala Val Arg Gly Asn Ala Ala Val Leu Asp Tyr Cys Arg Thr Ser
 20 25 30
 Val Ser Ala Leu Ser Gly Ala Thr Ala Gly Ile Leu Gly Leu Thr Gly
 25 35 40 45
 Leu Tyr Gly Phe Ile Phe Tyr Leu Leu Ala Ser Val Leu Leu Ser Leu
 50 55 60
 Leu Leu Ile Leu Lys Ala Gly Arg Arg Trp Asn Lys Tyr Phe Lys Ser
 65 70 75 80
 30 Arg Arg Pro Leu Phe Thr Gly Gly Leu Ile Gly Gly Leu Phe Thr Tyr
 85 90 95
 Val Leu Phe Trp Thr Phe Leu Tyr Gly Met Val His Val Tyr
 100 105 110

 35 <210> 128

147/177

<211> 91

<212> PRT

<213> Homo sapience

5 <400> 128

Met Val Tyr Ile Ser Asn Gly Gln Val Leu Asp Ser Arg Ser Gln Ser

1 5 10 15

Pro Trp Arg Leu Ser Leu Ile Thr Asp Phe Phe Trp Gly Ile Ala Glu

20 25 30

10 Phe Val Val Leu Phe Phe Lys Thr Leu Leu Gln Gln Asp Val Lys Lys

35 40 45

Arg Arg Ser Tyr Gly Asn Ser Ser Asp Ser Arg Tyr Asp Asp Gly Arg

50 55 60

Gly Pro Pro Gly Asn Pro Pro Arg Arg Met Gly Arg Ile Asn His Leu

15 65 70 75 80

Arg Gly Pro Ser Pro Pro Pro Met Ala Gly Gly

85 90

<210> 129

20 <211> 344

<212> PRT

<213> Homo sapience

<400> 129

25 Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser

1 5 10 15

Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu

20 25 30

Leu Leu Pro His Cys Gln Lys Leu Phe Val Tyr Asp Leu His Ala Val

30 35 40 45

Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys

50 55 60

Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe

65 70 75 80

35 Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu

148/177

	85	90	95
	Leu Gly Ser Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu		
	100	105	110
5	Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser		
	115	120	125
	Gly Phe Leu Ala Pro Val Phe Ala Leu Phe Val Pro Phe Tyr Cys Ser		
	130	135	140
	Ile Pro Arg Val Gln Val Ala Gln Ile Leu Gly Pro Leu Ser Ile Thr		
	145	150	155
10	Asn Lys Thr Leu Ile Tyr Ile Leu Gly Leu Gln Leu Phe Thr Ser Gly		
	165	170	175
	Ser Tyr Ile Trp Ile Val Ala Ile Ser Gly Leu Met Ser Gly Leu Cys		
	180	185	190
15	Tyr Asp Ser Lys Met Phe Gln Val His Gln Val Leu Cys Ile Pro Ser		
	195	200	205
	Trp Met Ala Lys Phe Phe Ser Trp Thr Leu Glu Pro Ile Phe Ser Ser		
	210	215	220
	Ser Glu Pro Thr Ser Glu Ala Arg Ile Gly Met Gly Ala Thr Leu Asp		
	225	230	235
20	Ile Gln Arg Gln Gln Arg Met Glu Leu Leu Asp Arg Gln Leu Met Phe		
	245	250	255
	Ser Gln Phe Ala Gln Gly Arg Arg Gln Arg Gln Gln Gln Gly Gly Met		
	260	265	270
	Ile Asn Trp Asn Arg Leu Phe Pro Pro Leu Arg Gln Arg Gln Asn Val		
25	275	280	285
	Asn Tyr Gln Gly Gly Arg Gln Ser Glu Pro Ala Ala Pro Pro Leu Glu		
	290	295	300
	Val Ser Glu Glu Gln Val Ala Arg Leu Met Glu Met Gly Phe Ser Arg		
	305	310	315
30	Gly Asp Ala Leu Glu Ala Leu Arg Ala Ser Asn Asn Asp Leu Asn Val		
	325	330	335
	Ala Thr Asn Phe Leu Leu Gln His		
	340		
35	<210> 130		

149/177

<211> 428

<212> PRT

<213> Homo sapience

5

<400> 130

Met	Gly	Pro	Pro	Pro	Gly	Ala	Gly	Val	Ser	Cys	Arg	Gly	Gly	Cys	Gly	
1				5					10					15		
Phe	Ser	Arg	Leu	Leu	Ala	Trp	Cys	Phe	Leu	Leu	Ala	Leu	Ser	Pro	Gln	
			20				25						30			
10	Ala	Pro	Gly	Ser	Arg	Gly	Ala	Glu	Ala	Val	Trp	Thr	Ala	Tyr	Leu	Asn
			35				40						45			
Val	Ser	Trp	Arg	Val	Pro	His	Thr	Gly	Val	Asn	Arg	Thr	Val	Trp	Glu	
		50				55				60						
Leu	Ser	Glu	Glu	Gly	Val	Tyr	Gly	Gln	Asp	Ser	Pro	Leu	Glu	Pro	Val	
15	65				70				75				80			
Ala	Gly	Val	Leu	Val	Pro	Pro	Asp	Gly	Pro	Gly	Ala	Leu	Asn	Ala	Cys	
				85					90				95			
Asn	Pro	His	Thr	Asn	Phe	Thr	Val	Pro	Thr	Val	Trp	Gly	Ser	Thr	Val	
			100					105					110			
20	Gln	Val	Ser	Trp	Leu	Ala	Leu	Ile	Gln	Arg	Gly	Gly	Gly	Cys	Thr	Phe
			115					120					125			
Ala	Asp	Lys	Ile	His	Leu	Ala	Tyr	Glu	Arg	Gly	Ala	Ser	Gly	Ala	Val	
		130				135					140					
Ile	Phe	Asn	Phe	Pro	Gly	Thr	Arg	Asn	Glu	Val	Ile	Pro	Met	Ser	His	
25	145				150				155				160			
Pro	Gly	Ala	Val	Asp	Ile	Val	Ala	Ile	Met	Ile	Gly	Asn	Leu	Lys	Gly	
			165					170				175				
Thr	Lys	Ile	Leu	Gln	Ser	Ile	Gln	Arg	Gly	Ile	Gln	Val	Thr	Met	Val	
			180					185				190				
30	Ile	Glu	Val	Gly	Lys	Lys	His	Gly	Pro	Trp	Val	Asn	His	Tyr	Ser	Ile
			195					200				205				
Phe	Phe	Val	Ser	Val	Ser	Phe	Phe	Ile	Ile	Thr	Ala	Ala	Thr	Val	Gly	
		210				215				220						
Tyr	Phe	Ile	Phe	Tyr	Ser	Ala	Arg	Arg	Leu	Arg	Asn	Ala	Arg	Ala	Gln	
35	225					230				235			240			

	Ser Arg Lys Gln Arg Gln Leu Lys Ala Asp Ala Lys Lys Ala Ile Gly			
	245	250	255	
	Arg Leu Gln Leu Arg Thr Leu Lys Gln Gly Asp Lys Glu Ile Gly Pro			
	260	265	270	
5	Asp Gly Asp Ser Cys Ala Val Cys Ile Glu Leu Tyr Lys Pro Asn Asp			
	275	280	285	
	Leu Val Arg Ile Leu Thr Cys Asn His Ile Phe His Lys Thr Cys Val			
	290	295	300	
	Asp Pro Trp Leu Leu Glu His Arg Thr Cys Pro Met Cys Lys Cys Asp			
10	305	310	315	320
	Ile Leu Lys Ala Leu Gly Ile Glu Val Asp Val Glu Asp Gly Ser Val			
	325	330	335	
	Ser Leu Gln Val Pro Val Ser Asn Glu Ile Ser Asn Ser Ala Ser Ser			
	340	345	350	
15	His Glu Glu Asp Asn Arg Ser Glu Thr Ala Ser Ser Gly Tyr Ala Ser			
	355	360	365	
	Val Gln Gly Thr Asp Glu Pro Pro Leu Glu Glu His Val Gln Ser Thr			
	370	375	380	
	Asn Glu Ser Leu Gln Leu Val Asn His Glu Ala Asn Ser Val Ala Val			
20	385	390	395	400
	Asp Val Ile Pro His Val Asp Asn Pro Thr Phe Glu Glu Asp Glu Thr			
	405	410	415	
	Pro Asn Gln Glu Thr Ala Val Arg Glu Ile Lys Ser			
	420	425		
25				
	<210> 131			
	<211> 1449			
	<212> DNA			
	<213> Homo sapience			
30				
	<400> 131			
	atgaaagcct tccacacttt ctgtgttgtc cttctggtgt ttgggagtgt ctctgaagcc	60		
	aagtttgatg attttgagga tgaggaggac atagtagagt atgatgataa tgacttcgct	120		
	gaatttgagg atgtcatgga agactctgtt actgaatctc ctcaacgggt cataatcact	180		
35	qaaqatgatq aaqatqaqac cactgtggaq ttggaagggc aggatgaaaa ccaagaagga	240		

151/177

	gattttgaag atgcagatac ccaggagggg gatactgaga gtgaaccata tgatgatgaa	300
	gaatttgaag gttatgaaga caaaccagat acttcttcta gcaaaaataa agacccaata	360
	acgattgttg atgttcctgc acacctccag aacagctggg agagttatta tctagaaatt	420
	ttgatggtga ctggtctgct tgettatact atgaattaca tcattgggaa gaataaaaac	480
5	agtcgccttg cacaggcctg gtttaacact catagggagc ttttggagag caactttact	540
	ttagtggggg atgatggaac taacaaagaa gccacaagca caggaaagtt gaaccaggag	600
	aatgagcaca tctataacct gtggtgttct ggtcgagtgt gctgtgaggg catgcttact	660
	cagctgaggt tcctcaagag acaagactta ctgaatgtcc tggcccggat gatgaggcca	720
	gtgagtgatc aagtgc aaat aaaagtaacc atgaatgatg aagacatgga tacctacgta	780
10	tttgcgtgtg gcacacggaa agccttggtg cgactacaga aagagatgca ggatttgagt	840
	gagttttgta gtgataaacc taagtctgga gcaaagtatg gactgccgga ctctttggcc	900
	atcctgtcag agatgggaga agtcacagac ggaatgatgg atacaaagat ggttcacttt	960
	cttacacact atgctgacaa gattgaatct gttcattttt cagaccagtt ctctggtcca	1020
	aaaattatgc aagaggaagg tcagccttta aagctacctg acactaagag gacactgttg	1080
15	tttacattta atgtgcctgg ctcaggtaac acttacccaa aggatatgga ggcactgcta	1140
	cccctgatga acatggtgat ttattctatt gataaagcca aaaagttccg actcaacaga	1200
	gaaggc aaac aaaaagcaga taagaaccgt gcccgagtag aagagaactt cttgaaactg	1260
	acacatgtgc aaagacagga agcagcacag tctcggcggg aggagaaaaa aagagcagag	1320
	aaggagcgaa tcatgaatga ggaagatcct gagaaacagc gcaggctgga ggaggctgca	1380
20	ttgaggcgtg agcaaaagaa gttggaaaag aagcaaatga aaatgaaaca aatcaaagtg	1440
	aaagccatg	1449
	<210> 132	
	<211> 1002	
25	<212> DNA	
	<213> Homo sapience	
	<400> 132	
	atggtagagt tcgcgccctt gtttatgccg tgggagcgca ggctgcagac acttgcgtgc	60
30	ctacagtttg tcttctcctt cttggcactg gccgagatct gcactgtggg cttcatagcc	120
	ctcctgttta caagattctg gctcctcact gtctgtatg cggcctggtg gtatctggac	180
	cgagacaagc cacggcaggg gggccggcac atccaggcca tcagggtgctg gactatatgg	240
	aagtacatga aggactatct ccccatctcg ctggtcaaga ctgctgagct ggacccctct	300
	cggaactaca ttgcgggctt ccacccccat ggagtctgg cagtcggagc ctttgccaac	360
35	ctgtgcactg agagcacagg cttctcttcg atcttccccg gtatccgccc ccatctgatg	420

152/177

atgetgacct tgtggttcg ggccecttc ttcagagatt acatcatgtc tgcagggttg 480
 gtcacatcag aaaaggagag tgctgtcac attctgaaca ggaagggttg cggaaacttg 540
 ctgggcatca ttgtagggg tgcccaggag gccctggatg ccaggccttg atccttcacg 600
 ctgttactgc ggaaccgaaa gggcttcgtc aggctcgccc tgacacacgg ggcacccctg 660
 5 gtgccaatct tctccttcgg ggagaatgac ctatttgacc agattcccaa ctctttctggc 720
 tcctgggttac gctatatcca gaatcggttg cagaagatca tgggcatctc cctcccactc 780
 tttcatggcc gtggtgtctt ccagtacagc tttggtttaa taccctaccg ccggcccactc 840
 accactgttg tggggaagcc catcgaggta cagaagacgc tgcacccctc ggaggaggag 900
 gtgaaccagc tgcaccagcg ttatatcaaa gagctgtgca acctcttcga ggcccacaaa 960
 10 ctttaagttca acatccctgc tgaccagcac ttggagttct gc 1002

<210> 133

<211> 801

<212> DNA

15 <213> Homo sapience

<400> 133

atggcgccct gggcgctcct cagccctggg gtccctggtgc ggaccgggca caccgtgctg 60
 acctggggaa tcaogctggt gctcttctctg cagcataccg agctgaggca atgggaggag 120
 20 cagggggagc tgetcctgce cctcaccttc ctgctcctgg tgetgggctc cctgctgctc 180
 tacctcctg tgtcactcat ggaccctggc tacgtgaatg tgcagcccca gcctcaggag 240
 gagctcaaag aggagcagac agccatggtt cctccagcca tccctcttcg gcgctgcaga 300
 tactgcctgg tgetgcagcc cctgagggct cggcactgce gtgagtgcg ccgttgctc 360
 cgccgctacg accaccactg cccctggatg gagaactgtg tgggagagcg caaccaccca 420
 25 ctctttgttg tctacctggc gctgcagctg gtggtgcttc tgtggggcct gtacctggca 480
 tggtcaggcc tccggttctt ccagccctgg ggtctgtggt tgcgggtccag cgggctcctg 540
 ttegccacct tctgctgct gtccctcttc tcgttggtgg ccagcctgct cctcgtctcg 600
 cacctctacc tgggtggccag caacaccacc acctgggaat tcctctctc acaccgcatc 660
 gcctatctcc gccagcgccc cagcaacccc ttcgaccgag gcctgacccg caacctggcc 720
 30 cacttcttct gtggatggcc ctcagggtcc tgggagaccc tctgggctga ggaggaggaa 780
 gagggcagca gccagctgt t 801

<210> 134

<211> 318

35 <212> DNA

153/177

<213> Homo sapience

<400> 134

5 atgtccacta acaatatgtc ggacccacgg aggccgaaca aagtgtgtgag gtacaagccc 60
 ccgccgagcg aatgtaaccc ggcccttgac gacccgacgc cggactacat gaacctgtgtg 120
 ggcattgatct tcagcatgtg cggcctcatg cttaagctga agtgggtgtgc ttgggtgctg 180
 gtctactgtc ccttcattcag ctttgccaac tctcggagct cggaggacac gaagcaaatg 240
 atgagtagct tcatgtgtgc catctctgcc gtggtgatgt cctatctgca gaatectcag 300
 cccatgacgc ccccatgg 318

10

<210> 135

<211> 672

<212> DNA

<213> Homo sapience

15

<400> 135

20 atgacctgt ttcacttcgg gaactgtctc gctcttgcct acttccccta cttcatcacc 60
 tacaagtga ggggcctgtc cgagtacaac gccttctgga aatgcgtcca ggctggagtc 120
 acctacctct ttgtccaact ctgcaagatg ctgttcttgg ccactttctt tcccacctgg 180
 gaaggcggca tctatgactt cattggggag ttcattgaagg ccagcgtgga tgtggcagac 240
 ctgataggtc taaaccttgt catgtcccg aatgccggca agggagagta caagatcatg 300
 gttgtgtccc tgggtgtggc cactgtgtgag cttattatgt cccgctgcat tcccctatgg 360
 gtcggagccc ggggcattga gtttgactgg aagtacatcc agatgagcat agactccaac 420
 atcagtctgg tccattacat cgtcgcgtct gctcaggtct ggatgataac acgctatgat 480
 25 ctgtaccaca ccttcgggcc agctgtcttc ctgtgtatgt tctcagtgct ctacaaggcc 540
 tttgttatgg agaccttctg ccacctctgc tcgtgtggga gttgggcagc tctactggcc 600
 cgagcagtggt taacggggct gctggccctc agcactttgg ccctgtatgt cgcggtgtgc 660
 aatgtgcact cc 672

30

<210> 136

<211> 774

<212> DNA

<213> Homo sapience

35

<400> 136

154/177

	atggcggtct tggcaacctct aattgctctc gtgtattcgg tgccgcgact ttcacgatgg	60
	ctcgcccaac cttactacct tctgtcggcc ctgctctctg ctgccttcct actcgtgagg	120
	aaactgcccgc cgctctgccca cgggtctgccc acccaacgcg aagacggtaa cccgtgtgac	180
	tttgactgga gagaagtgga gatcctgatg tttctcagtg ccattgtgat gatgaagaac	240
5	cgcagatcca tgttctgat gacgtgcaaa cccccctat atatgggccc tgagtatata	300
	aagtacttca atgataaaac cattgatgag gaactagaac gggacaagag ggtcacttgg	360
	attgtggagt tctttgccaa ttggtctaat gactgccaat catttgcccc tatctatgct	420
	gacctctccc ttaaatacaa ctgtacaggg ctaaattttg ggaagggtgga tgttggacgc	480
	tatactgatg ttagtacgcg gtacaaagtg agcacatcac cctcaccaa gcaactccct	540
10	accctgatec tgttccaagg tggcaaggag gcaatgcggc ggccacagat tgacaagaaa	600
	ggacgggctg tctcatggac cttctctgag gagaatgtga tccgagaatt taacttaaat	660
	gagctatacc agcggggccaa gaaactatca aaggctggag acaatatccc tgaggagcag	720
	cctgtggctt caacccccac cacagtgtca gatggggaaa acaagaagga taaa	774
15	<210> 137	
	<211> 330	
	<212> DNA	
	<213> Homo sapience	
20	<400> 137	
	atggccgcgg tggtagccaa gcgggaaggc ccgcggttca tcagcgaggc ggccgtgcgg	60
	ggcaacgcgc ccgtcctgga ttattgcgcg acctcggtgt cagcgctgtc gggggccacg	120
	gccggcatcc tcggcctcac cggcctctac ggcttcatct tctacctgct cgcctcgcgc	180
	ctgctctccc tgctcctcat tctcaaggcg ggaaggaggt ggaacaaata tttcaaatca	240
25	cggagacctc tctttacagg aggcctcatc gggggcctct tcacctacgt cctgttctgg	300
	acgttctctc acggcatggt gcacgtctac	330
	<210> 138	
	<211> 273	
30	<212> DNA	
	<213> Homo sapience	
	<400> 138	
	atggtttaca tctcgaacgg acaagtgttg gacagccgga gtcagtctcc atggagatta	60
35	tctttgataa cagatttctt ctgggggaata gctgagtttg tggttttgtt tttcaaaact	120

155/177

ctgcttcagc aagatgtgaa aaaaagaaga agctatggaa actcatctga ttccagatat 180
 gatgatggaa gagggccacc aggaaaccct ccccgaaaga tgggtagaat caatcatctg 240
 cgtggcccta gtccccctcc aatggctggt gga 273

5 <210> 139
 <211> 1032
 <212> DNA
 <213> Homo sapience

10 <400> 139
 atgttcacca gcaccggtc cagtgggtc tacaaggcgc ctctgtcgaa gagccttctg 60
 ctggtcccca gtgccctctc cctcctgctc gccctcctcc tgccctactg ccagaagctc 120
 tttgtgtatg accttcacgc agtcaagaac gacttcacaga tttggagggt gatatgtgga 180
 agaataattht gcccttgattht gaaagatact ttctgcagta gtctgcttat ttataattht 240
 15 aggataththt aaagaagata tggaagcaga aaaththtgc cctthththtgc gggthththtgc 300
 gththththtgc cctthththtga cththththtgc attgaagcta tgcagthththt cththththtgc 360
 actgcagcta gtaaththtgc ttctggattht ctggcacctg tgtthththtgc gththththtgc 420
 tththththtgc ccataccaag agtccaagtg gcacaaattht tgggtccgtht gtccatcaca 480
 aacaagacat tgatththtgc attgggactg cagctthththt cctctggthtgc ctacatctgg 540
 20 attgtagcca taagtggact tatgtccggt ctgtgctacg acagcaaat gththththtgc 600
 catcaggtgc tctgcatccc cagctggatg gcaaattht tththththtgc actthththtgc 660
 atctthththt cththththtgc caccagcgaa gccagaattht ggatgggagc cacgctggac 720
 atccagagac agcagagaat ggagctgctg gaccggcagc tgatgthththtgc tcaatthththtgc 780
 caagggaggc gacagagaca gcagcaggga ggaatgatca attggaatgc tctththththtgc 840
 25 cctththththtgc agcgacaaaa cgtaaactat cagggcggtc ggcagthththtgc gccagcagcg 900
 cccctcttag aagththththtgc ggaacaggtc gcccggtca tggagatggg atththththtgc 960
 ggtgatgctt tggaagccct gagagctthtca aacaatgacc tcaatgthththtgc caccaacttht 1020
 ctgctgcagc ac 1032

30 <210> 140
 <211> 1284
 <212> DNA
 <213> Homo sapience

35 <400> 140

156/177

	atggggccgc cgcctggggc cggggtctcc tgccgcgggtg gctgcggctt ttccagattg	60
	ctggcatggt gcttcttget ggccctgagt ccgcaggcac ccggttcccg gggggctgaa	120
	gcagtgtgga ccgcgtacct caacgtgtcc tggcgggttc cgcacacggg agtgaacctg	180
	acggtgtggg agctgagcga ggagggcggtg tacggccagg actcgcctgt ggagcctgtg	240
5	gctgggggtcc tgggtaccgcc cgacggggccc ggggcgctta acgcctgtaa cccgcacacg	300
	aatttcacgg tgccccacgg ttggggaagc accgtgcaag tctcttggtt ggccctcacc	360
	caacgcggcg ggggctgcac cttegcagac aagatccacc tggcttatga gagagggcg	420
	tctggagccg tcatctttaa cttccccggg acccgcaatg aggtcatccc catgtctcac	480
	ccgggtgcag tagacattgt tgcaatcatg atcggcaatc tgaaaggcac aaaaattctg	540
10	caatctattc aaagaggcat acaagtgaca atggtcatag aagtagggaa aaaacatggc	600
	ccttggggtga atcactatcc aatttttttc gtttctgtgt ctttttttat tattacggcg	660
	gcaactgtgg gctattttat cttttattct gctcgaaggc tacggaatgc aagagctcaa	720
	agcaggaagc agaggcaatt aaaggcagat gctaaaaaag ctattggaag gcttcaacta	780
	cgcacactga aacaaggaga caaggaaatt ggccctgatg gagatagttg tgctgtgtgc	840
15	attgaattgt ataaaccaa tgatttggtg cgcactctta cgtgcaacca tattttccat	900
	aagacatgtg ttgacctatg gctgttagaa cacaggactt gccccatgtg caaatgtgac	960
	atactcaaag ctttggggat tgaggtggat gttgaagatg gatcagtgtc tttaacaagtc	1020
	cctgtatcca atgaaatacc taatagtgcc tctcccatg aagaggataa tcgcagcgag	1080
	accgcatcat ctggatatgc ttcagtacag ggaacagatg aaccgcctct ggaggaacac	1140
20	gtgcagtcaa caaatgaaag tctacagctg gtaaaccatg aagcaaattc tgtggcagtg	1200
	gatgttatcc ctcatgttga caaccacaac tttgaagaag acgaaactcc taatcaagag	1260
	actgctgttc gagaaattaa atct	1284
	<210> 141	
25	<211> 2050	
	<212> DNA	
	<213> Homo sapiens	
	<220>	
	<221> CDS	
30	<222> (122)...(1573)	
	<400> 141	
	aaaaaacgc tgcatcgcg gaggcggcgg ccaggccgag aggcaggccg ggcaggggtg	60
	tggagcgag ggcgctggc cgggtttcgg cttcggccac agcttttttt ctcaaggtgc	120
35	a atg aaa gcc ttc cac act ttc tgt gtt gtc ctt ctg gtg ttt ggg	166

157/177

Met Lys Ala Phe His Thr Phe Cys Val Val Leu Leu Val Phe Gly

	1	5	10	15	
	agt gtc tct gaa gcc aag ttt gat gat ttt gag gat gag gag gac ata	214			
	Ser Val Ser Glu Ala Lys Phe Asp Asp Phe Glu Asp Glu Glu Asp Ile				
5		20	25	30	
	gta gag tat gat gat aat gac ttc gct gaa ttt gag gat gtc atg gaa	262			
	Val Glu Tyr Asp Asp Asn Asp Phe Ala Glu Phe Glu Asp Val Met Glu				
	35	40	45		
	gac tct gtt act gaa tct cct caa cgg gtc ata atc act gaa gat gat	310			
10	Asp Ser Val Thr Glu Ser Pro Gln Arg Val Ile Ile Thr Glu Asp Asp				
	50	55	60		
	gaa gat gag acc act gtg gag ttg gaa ggg cag gat gaa aac caa gaa	358			
	Glu Asp Glu Thr Thr Val Glu Leu Glu Gly Gln Asp Glu Asn Gln Glu				
	65	70	75		
15	gga gat ttt gaa gat gca gat acc cag gag gga gat act gag agt gaa	406			
	Gly Asp Phe Glu Asp Ala Asp Thr Gln Glu Gly Asp Thr Glu Ser Glu				
	80	85	90	95	
	cca tat gat gat gaa gaa ttt gaa ggt tat gaa gac aaa cca gat act	454			
	Pro Tyr Asp Asp Glu Glu Phe Glu Gly Tyr Glu Asp Lys Pro Asp Thr				
20		100	105	110	
	tct tct agc aaa aat aaa gac cca ata acg att gtt gat gtt cct gca	502			
	Ser Ser Ser Lys Asn Lys Asp Pro Ile Thr Ile Val Asp Val Pro Ala				
	115	120	125		
	cac etc cag aac agc tgg gag agt tat tat cta gaa att ttg atg gtg	550			
25	His Leu Gln Asn Ser Trp Glu Ser Tyr Tyr Leu Glu Ile Leu Met Val				
	130	135	140		
	act ggt ctg ctt gct tat atc atg aat tac atc att ggg aag aat aaa	598			
	Thr Gly Leu Leu Ala Tyr Ile Met Asn Tyr Ile Ile Gly Lys Asn Lys				
	145	150	155		
30	aac agt cgc ctt gca cag gcc tgg ttt aac act cat agg gag ctt ttg	646			
	Asn Ser Arg Leu Ala Gln Ala Trp Phe Asn Thr His Arg Glu Leu Leu				
	160	165	170	175	
	gag agc aac ttt act tta gtg ggg gat gat gga act aac aaa gaa gcc	694			
	Glu Ser Asn Phe Thr Leu Val Gly Asp Asp Gly Thr Asn Lys Glu Ala				
35		180	185	190	

158/177

	aca agc aca gga aag ttg aac cag gag aat gag cac atc tat aac ctg	742
	Thr Ser Thr Gly Lys Leu Asn Gln Glu Asn Glu His Ile Tyr Asn Leu	
	195 200 205	
	tgg tgt tct ggt cga gtg tgc tgt gag ggc atg ctt atc cag ctg agg	790
5	Trp Cys Ser Gly Arg Val Cys Cys Glu Gly Met Leu Ile Gln Leu Arg	
	210 215 220	
	ttc ctc aag aga caa gac tta ctg aat gtc ctg gcc cgg atg atg agg	838
	Phe Leu Lys Arg Gln Asp Leu Leu Asn Val Leu Ala Arg Met Met Arg	
	225 230 235	
10	cca gtg agt gat caa gtg caa ata aaa gta acc atg aat gat gaa gac	886
	Pro Val Ser Asp Gln Val Gln Ile Lys Val Thr Met Asn Asp Glu Asp	
	240 245 250 255	
	atg gat acc tac gta ttt gct gtt ggc aca cgg aaa gcc ttg gtg cga	934
	Met Asp Thr Tyr Val Phe Ala Val Gly Thr Arg Lys Ala Leu Val Arg	
15	260 265 270	
	cta cag aaa gag atg cag gat ttg agt gag ttt tgt agt gat aaa cct	982
	Leu Gln Lys Glu Met Gln Asp Leu Ser Glu Phe Cys Ser Asp Lys Pro	
	275 280 285	
	aag tct gga gca aag tat gga ctg ccg gac tct ttg gcc atc ctg tca	1030
20	Lys Ser Gly Ala Lys Tyr Gly Leu Pro Asp Ser Leu Ala Ile Leu Ser	
	290 295 300	
	gag atg gga gaa gtc aca gac gga atg atg gat aca aag atg gtt cac	1078
	Glu Met Gly Glu Val Thr Asp Gly Met Met Asp Thr Lys Met Val His	
	305 310 315	
25	ttt ctt aca cac tat gct gac aag att gaa tct gtt cat ttt tca gac	1126
	Phe Leu Thr His Tyr Ala Asp Lys Ile Glu Ser Val His Phe Ser Asp	
	320 325 330 335	
	cag ttc tct ggt cca aaa att atg caa gag gaa ggt cag cct tta aag	1174
	Gln Phe Ser Gly Pro Lys Ile Met Gln Glu Glu Gly Gln Pro Leu Lys	
30	340 345 350	
	cta cct gac act aag agg aca ctg ttg ttt aca ttt aat gtg cct ggc	1222
	Leu Pro Asp Thr Lys Arg Thr Leu Leu Phe Thr Phe Asn Val Pro Gly	
	355 360 365	
	tca ggt aac act tac cca aag gat atg gag gca ctg cta ccc ctg atg	1270
35	Ser Gly Asn Thr Tyr Pro Lys Asp Met Glu Ala Leu Leu Pro Leu Met	

159/177

	370	375	380	
	aac atg gtg att tat tct att gat aaa gcc aaa aag ttc cga ctc aac			1318
	Asn Met Val Ile Tyr Ser Ile Asp Lys Ala Lys Lys Phe Arg Leu Asn			
	385	390	395	
5	aga gaa ggc aaa caa aaa gca gat aag aac cgt gcc cga gta gaa gag			1366
	Arg Glu Gly Lys Gln Lys Ala Asp Lys Asn Arg Ala Arg Val Glu Glu			
	400	405	410	415
	aac ttc ttg aaa ctg aca cat gtg caa aga cag gaa gca gca cag tct			1414
	Asn Phe Leu Lys Leu Thr His Val Gln Arg Gln Glu Ala Ala Gln Ser			
10	420	425	430	
	cgg cgg gag gag aaa aaa aga gca gag aag gag cga atc atg aat gag			1462
	Arg Arg Glu Glu Lys Lys Arg Ala Glu Lys Glu Arg Ile Met Asn Glu			
	435	440	445	
	gaa gat cct gag aaa cag cgc agg ctg gag gag gct gca ttg agg cgt			1510
15	Glu Asp Pro Glu Lys Gln Arg Arg Leu Glu Glu Ala Ala Leu Arg Arg			
	450	455	460	
	gag caa aag aag ttg gaa aag aag caa atg aaa atg aaa caa atc aaa			1558
	Glu Gln Lys Lys Leu Glu Lys Lys Gln Met Lys Met Lys Gln Ile Lys			
	465	470	475	
20	gtg aaa gcc atg taaagccatc ccagagattt gagttctgat gccacctgta			1610
	Val Lys Ala Met			
	480			
	agctctgaat tcacaggaaa catgaaaaac gccagtccat ttctcaacct taaatttcag			1670
	acagtcttgg gcaactgaga aatccttatt tcatacatcta ctctgtttgg gggttgggggt			1730
25	tttacagaga ttgaagatac ctggaaaggg ctctgtttca agaatttttt tttccagata			1790
	atcaaattat ttgattatt ttataaaagg aatgatctat gaaatctgtg taggttttaa			1850
	atattttaaa aattataata caaatcatca gtgttttttag tacttcagtg tttaaagaaa			1910
	taccatgaaa tttataggta gataaccaga ttgttgcttt ttgttttaaac caagcagttg			1970
	aaatggctat aaagactgac tctaaaccaa gattctgcaa ataatgattg gaattgcaca			2030
30	ataaacattg cttgatgttt			2050
	<210> 142			
	<211> 2746			
	<212> DNA			
35	<213> Homo sapience			

160/177

<220>

<221> CDS

<222> (70)...(1074)

5 <400> 142

aaaacctgtg ggtgcctcag accacagcag agctcacaga acctgcggga gccaggctga 60

cccgccagc atg gta gag ttc gcg ccc ttg ttt atg ccg tgg gag cgc 108

Met Val Glu Phe Ala Pro Leu Phe Met Pro Trp Glu Arg

1

5

10

10 agg ctg cag aca ctt gct gtc cta cag ttt gtc ttc tcc ttc ttg gca 156

Arg Leu Gln Thr Leu Ala Val Leu Gln Phe Val Phe Ser Phe Leu Ala

15

20

25

ctg gcc gag atc tgc act gtg ggc ttc ata gcc ctc ctg ttt aca aga 204

Leu Ala Glu Ile Cys Thr Val Gly Phe Ile Ala Leu Leu Phe Thr Arg

15 30 35 40 45

ttc tgg ctc ctc act gtc ctg tat gcg gcc tgg tgg tat ctg gac cga 252

Phe Trp Leu Leu Thr Val Leu Tyr Ala Ala Trp Trp Tyr Leu Asp Arg

50

55

60

gac aag cca cgg cag ggg ggc cgg cac atc cag gcc atc agg tgc tgg 300

20 Asp Lys Pro Arg Gln Gly Gly Arg His Ile Gln Ala Ile Arg Cys Trp

65

70

75

act ata tgg aag tac atg aag gac tat ttc ccc atc tcg ctg gtc aag 348

Thr Ile Trp Lys Tyr Met Lys Asp Tyr Phe Pro Ile Ser Leu Val Lys

80

85

90

25 act gct gag ctg gac ccc tct cgg aac tac att gcg ggc ttc cac ccc 396

Thr Ala Glu Leu Asp Pro Ser Arg Asn Tyr Ile Ala Gly Phe His Pro

95

100

105

cat gga gtc ctg gca gtc gga gcc ttt gcc aac ctg tgc act gag agc 444

His Gly Val Leu Ala Val Gly Ala Phe Ala Asn Leu Cys Thr Glu Ser

30 110 115 120 125

aca ggc ttc tct tcg atc ttc ccc ggt atc cgc ccc cat ctg atg atg 492

Thr Gly Phe Ser Ser Ile Phe Pro Gly Ile Arg Pro His Leu Met Met

130

135

140

ctg acc ttg tgg ttc cgg gcc ccc ttc ttc aga gat tac atc atg tct 540

35 Leu Thr Leu Trp Phe Arg Ala Pro Phe Phe Arg Asp Tyr Ile Met Ser

161/177

	145	150	155	
	gca ggg ttg gtc aca tca gaa aag gag agt gct gct cac att ctg aac			588
	Ala Gly Leu Val Thr Ser Glu Lys Glu Ser Ala Ala His Ile Leu Asn			
	160	165	170	
5	agg aag ggt ggc gga aac ttg ctg ggc atc att gta ggg ggt gcc cag			636
	Arg Lys Gly Gly Gly Asn Leu Leu Gly Ile Ile Val Gly Gly Ala Gln			
	175	180	185	
	gag gcc ctg gat gcc agg cct gga tcc ttc acg ctg tta ctg cgg aac			684
	Glu Ala Leu Asp Ala Arg Pro Gly Ser Phe Thr Leu Leu Leu Arg Asn			
10	190	195	200	205
	cga aag ggc ttc gtc agg ctc gcc ctg aca cac ggg gca ccc ctg gtg			732
	Arg Lys Gly Phe Val Arg Leu Ala Leu Thr His Gly Ala Pro Leu Val			
	210	215	220	
	cca atc ttc tcc ttc ggg gag aat gac cta ttt gac cag att ccc aac			780
15	Pro Ile Phe Ser Phe Gly Glu Asn Asp Leu Phe Asp Gln Ile Pro Asn			
	225	230	235	
	tct tct ggc tcc tgg tta cgc tat atc cag aat cgg ttg cag aag atc			828
	Ser Ser Gly Ser Trp Leu Arg Tyr Ile Gln Asn Arg Leu Gln Lys Ile			
	240	245	250	
20	atg ggc atc tcc ctc cca ctc ttt cat ggc cgt ggt gtc ttc cag tac			876
	Met Gly Ile Ser Leu Pro Leu Phe His Gly Arg Gly Val Phe Gln Tyr			
	255	260	265	
	agc ttt ggt tta ata ccc tac cgc cgg ccc atc acc act gtg gtg ggg			924
	Ser Phe Gly Leu Ile Pro Tyr Arg Arg Pro Ile Thr Thr Val Val Gly			
25	270	275	280	285
	aag ccc atc gag gta cag aag acg ctg cat ccc tcg gag gag gag gtg			972
	Lys Pro Ile Glu Val Gln Lys Thr Leu His Pro Ser Glu Glu Glu Val			
	290	295	300	
	aac cag ctg cac cag cgt tat atc aaa gag ctg tgc aac ctc ttc gag			1020
30	Asn Gln Leu His Gln Arg Tyr Ile Lys Glu Leu Cys Asn Leu Phe Glu			
	305	310	315	
	gcc cac aaa ctt aag ttc aac atc cct gct gac cag cac ttg gag ttc			1068
	Ala His Lys Leu Lys Phe Asn Ile Pro Ala Asp Gln His Leu Glu Phe			
	320	325	330	
35	tgc tgagcccaa agggcagggc caacattagg gagccagca ggaggtgctg			1120

162/177

Cys

	tgctgagaag	acttcctgga	ggtgtttgtt	gaacatatct	gcagagcctt	cccagactcc	1180
	tgcaaatcca	acccatatca	ggtgttaagt	cagagcaggc	aatgcagaag	aggagaccag	1240
	accaaggggt	cagctggggc	taggacagtg	agggctgcta	gaggggctgg	gcctctcttt	1300
5	gcacatggac	actgggcccc	tctctatatt	gagtggctctg	ttaacattca	ttggtggctg	1360
	attccaaaag	atgagageca	aagctgcacg	gactcgagtc	ctaggctgca	cacctcacia	1420
	gcctctcttc	tactgcattc	tggtggctga	agcaagtcac	aaccagcag	attcaaggag	1480
	taaggaatag	gatccccctc	tggatgggag	gagcagcaat	gtcatattac	aaaaggggtg	1540
	ggacacatgc	agggattctt	actgccgtct	ttgcaaacia	tccacaaaaa	cttaaaaaact	1600
10	aaaagcctga	agcacaagca	ctctccaccc	caggcacaca	caccctggaa	ttccctgtgt	1660
	gacctgggta	ccaccactgt	gtgtcccgag	gatcccgag	cagctttgca	tcgctgccct	1720
	atctccctct	cgtctctccc	tggtgatccc	tcctgcacag	ccacagcgag	ctgtctaaaa	1780
	cacaaagctg	accgcgccat	ttctactca	gcctctctcc	atgacctccc	attgtctcta	1840
	ggataggggt	tggaccagtc	tgaatccaga	ggatcaggat	ccagcaggaa	ccagaggata	1900
15	atgtgaggag	ggtttaaaaa	ggaaccattt	tttgagggtg	gtgactgtt	tccacctga	1960
	ggcctggaag	gatgaatgga	agcagcagtt	cctgaaccag	gaagactcat	gtgtgggggc	2020
	cattgtctgt	caaggggcac	gaacaggtct	ggtgacctg	caagggagga	gccaggagca	2080
	agcattccca	cttcaccttc	ctccattcag	tctgtgccca	agttccccac	tgctgagccc	2140
	caactagaag	ctggagggaa	ggagggcctg	tggtctcagt	ccaggcatgt	aggcctcctg	2200
20	ggaaagggag	aatggcaaag	acaggcagag	tggatctgga	gggtcaacg	gaagacggaa	2260
	catgtccact	tccagggccg	agcttctcag	cctgccgttt	gccactctcc	agcatctggc	2320
	ccagcctgtc	catctctatc	tctcttcttc	ccttactccg	tgctcccatc	actcggaacc	2380
	atgtgcattt	ctttgtctca	gctatattgt	ctcacctctg	agtttttgcc	catgatgttg	2440
	gatgccatgg	aatgccatat	cctccccatt	atctccccct	tgtctggata	attcctactc	2500
25	atcctacaat	actgatttta	tctgtgcaaa	gaagtcttcc	ccagtgcctc	tggttgacag	2560
	gggtttcttc	tggtttctcc	agactttctg	ttcctccacc	acagccctta	gcacctggg	2620
	gaggaggtgt	tgctgtccag	gtaaatgtg	cgccaatgcc	cctgcctcta	gtgactcccc	2680
	tccagcctac	ccacaaacag	gacctgcctc	ctgtctcaca	aataaaaactg	aactcttgaa	2740
	atgggtg						2746

30

<210> 143

<211> 1136

<212> DNA

<213> Homo sapiens

35

<220>

163/177

<221> CDS

<222> (32)...(835)

<400> 143

5	attcttcctcggtgtggggccccgggcccagagggc g atg gcg ccc tgg gcg ctc ctc	52
	Met Ala Pro Trp Ala Leu Leu	
	1 5	
	agc cct ggg gtc ctg gtg cgg acc ggg cac acc gtg ctg acc tgg gga	100
	Ser Pro Gly Val Leu Val Arg Thr Gly His Thr Val Leu Thr Trp Gly	
10	10 15 20	
	atc acg ctg gtg ctc ttc ctg cac gat acc gag ctg cgg caa tgg gag	148
	Ile Thr Leu Val Leu Phe Leu His Asp Thr Glu Leu Arg Gln Trp Glu	
	25 30 35	
	gag cag ggg gag ctg ctc ctg ccc ctc acc ttc ctg ctc ctg gtg ctg	196
15	Glu Gln Gly Glu Leu Leu Leu Pro Leu Thr Phe Leu Leu Leu Val Leu	
	40 45 50 55	
	ggc tcc ctg ctg ctc tac ctc gct gtg tca ctc atg gac cct ggc tac	244
	Gly Ser Leu Leu Leu Tyr Leu Ala Val Ser Leu Met Asp Pro Gly Tyr	
	60 65 70	
20	gtg aat gtg cag ccc cag cct cag gag gag ctc aaa gag gag cag aca	292
	Val Asn Val Gln Pro Gln Pro Gln Glu Leu Lys Glu Glu Gln Thr	
	75 80 85	
	gcc atg gtt cct cca gcc atc cct ctt cgg cgc tgc aga tac tgc ctg	340
	Ala Met Val Pro Pro Ala Ile Pro Leu Arg Arg Cys Arg Tyr Cys Leu	
25	90 95 100	
	gtg ctg cag ccc ctg agg gct cgg cac tgc cgt gag tgc cgc cgt tgc	388
	Val Leu Gln Pro Leu Arg Ala Arg His Cys Arg Glu Cys Arg Arg Cys	
	105 110 115	
	gtc cgc cgc tac gac cac cac tgc ccc tgg atg gag aac tgt gtg gga	436
30	Val Arg Arg Tyr Asp His His Cys Pro Trp Met Glu Asn Cys Val Gly	
	120 125 130 135	
	gag cgc aac cac cca ctc ttt gtg gtc tac ctg gcg ctg cag ctg gtg	484
	Glu Arg Asn His Pro Leu Phe Val Val Tyr Leu Ala Leu Gln Leu Val	
	140 145 150	
35	gtg ctt ctg tgg ggc ctg tac ctg gca tgg tca ggc ctc cgg ttc ttc	532

164/177

	Val Leu Leu Trp Gly Leu Tyr Leu Ala Trp Ser Gly Leu Arg Phe Phe	
	155 160 165	
	cag ccc tgg ggt ctg tgg ttg cgg tcc agc ggg ctc ctg ttc gcc acc	580
	Gln Pro Trp Gly Leu Trp Leu Arg Ser Ser Gly Leu Leu Phe Ala Thr	
5	170 175 180	
	ttc ctg ctg ctg tcc ctc ttc tcg ttg gtg gcc agc ctg ctc ctc gtc	628
	Phe Leu Leu Leu Ser Leu Phe Ser Leu Val Ala Ser Leu Leu Leu Val	
	185 190 195	
	tcg cac ctc tac ctg gtg gcc agc aac acc acc acc tgg gaa ttc atc	676
10	Ser His Leu Tyr Leu Val Ala Ser Asn Thr Thr Thr Trp Glu Phe Ile	
	200 205 210 215	
	tcc tca cac cgc atc gcc tat ctc cgc cag cgc ccc agc aac ccc ttc	724
	Ser Ser His Arg Ile Ala Tyr Leu Arg Gln Arg Pro Ser Asn Pro Phe	
	220 225 230	
15	gac cga ggc ctg acc cgc aac ctg gcc cac ttc ttc tgt gga tgg ccc	772
	Asp Arg Gly Leu Thr Arg Asn Leu Ala His Phe Phe Cys Gly Trp Pro	
	235 240 245	
	tca ggg tcc tgg gag acc ctc tgg gct gag gag gag gaa gag ggc agc	820
	Ser Gly Ser Trp Glu Thr Leu Trp Ala Glu Glu Glu Glu Glu Gly Ser	
20	250 255 260	
	agc cca gct gtt tagggttgct ggaggccggg ctaccgtctt gtgcctga	870
	Ser Pro Ala Val	
	265	
	aaaccaagg ggcctgtcccc agctggggtg agcgcctcaga gggcctgggg cccctcactcc	930
25	tgccccagcc tcccagaccc cagaacggag cttcaagtca gacagatccc tgccttggtg	990
	ggcagttctg ccttccaagg aagaagggga agaaaaggac ctgtgggtgg ctcaggccca	1050
	agcagacccc gggetccacc ccagcccccgc ccaggctgct gccagtgcac actttttacaa	1110
	atttaatatata aagcaagtcc agtctt	1136
30	<210> 144	
	<211> 619	
	<212> DNA	
	<213> Homo sapience	
	<220>	
35	<221> CDS	

165/177

<222> (13)...(333)

<400> 144

5	cttcgactcg ct atg tcc act aac aat atg tcg gac cca cgg agg ccg	48
	Met Ser Thr Asn Asn Met Ser Asp Pro Arg Arg Pro	
	1 5 10	
	aac aaa gtg ctg agg tac aag ccc ccg ccg agc gaa tgt aac ccg gcc	96
	Asn Lys Val Leu Arg Tyr Lys Pro Pro Pro Ser Glu Cys Asn Pro Ala	
	15 20 25	
10	ttg gac gac ccg acg ccg gac tac atg aac ctg ctg ggc atg atc ttc	144
	Leu Asp Asp Pro Thr Pro Asp Tyr Met Asn Leu Leu Gly Met Ile Phe	
	30 35 40	
	agc atg tgc ggc ctc atg ctt aag ctg aag tgg tgt gct tgg gtc gct	192
	Ser Met Cys Gly Leu Met Leu Lys Leu Lys Trp Cys Ala Trp Val Ala	
15	45 50 55 60	
	gtc tac tgc tcc ttc atc agc ttt gcc aac tct cgg agc tcg gag gac	240
	Val Tyr Cys Ser Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp	
	65 70 75	
	acg aag caa atg atg agt agc ttc atg ctg tcc atc tct gcc gtg gtg	288
20	Thr Lys Gln Met Met Ser Ser Phe Met Leu Ser Ile Ser Ala Val Val	
	80 85 90	
	atg tcc tat ctg cag aat cct cag ccc atg acg ccc cca tgg	340
	Met Ser Tyr Leu Gln Asn Pro Gln Pro Met Thr Pro Pro Trp	
	95 100 105	
25	tgataccagc ctagaagggt cacatttttg accctgtcta tccactaggc ctgggctttg	390
	gctgctaaac ctgctgcctt cagctgccat cctggacttc cctgaatgag gccgtctcgg	450
	tgccccccagc tggatagagg gaacctggcc ctttcttagg gaacacccta ggcttaccoc	510
	tcctgcctcc ctccccctgc ctgctgctgg gggagatgct gtccatgttt ctaggggtat	570
	tcatttgctt tctcgttgaa acctgttggt aataaagttt ttcactcag	619
30		

<210> 145

<211> 864

<212> DNA

<213> Homo sapience

35 <220>

166/177

<221> CDS

<222> (111)...(785)

<400> 145

5	agg	tgg	gtg	cag	gcc	ctg	cgt	ggc	gaa	aga	gcc	ggc	gag	ccg	gga	ccc	gtc	ccc		60
	gag	acg	ccg	ctc	gcg	atc	ccg	cgg	ggc	ggg	acc	ggg	gcg	cat	atg	acc		116		
																	Met Thr			
																	1			
	ctg	ttt	cac	ttc	ggg	aac	tgc	ttc	gct	ctt	gcc	tac	ttc	ccc	tac	ttc		164		
10	Leu	Phe	His	Phe	Gly	Asn	Cys	Phe	Ala	Leu	Ala	Tyr	Phe	Pro	Tyr	Phe				
																	5 10 15			
	atc	acc	tac	aag	tgc	agc	ggc	ctg	tcc	gag	tac	aac	gcc	ttc	tgg	aaa		212		
	Ile	Thr	Tyr	Lys	Cys	Ser	Gly	Leu	Ser	Glu	Tyr	Asn	Ala	Phe	Trp	Lys				
																	20 25 30			
15	tgc	gtc	cag	gct	gga	gtc	acc	tac	ctc	ttt	gtc	caa	ctc	tgc	aag	atg		260		
	Cys	Val	Gln	Ala	Gly	Val	Thr	Tyr	Leu	Phe	Val	Gln	Leu	Cys	Lys	Met				
																	35 40 45 50			
	ctg	ttc	ttg	gcc	act	ttc	ttt	ccc	acc	tgg	gaa	ggc	ggc	atc	tat	gac		308		
	Leu	Phe	Leu	Ala	Thr	Phe	Phe	Pro	Thr	Trp	Glu	Gly	Gly	Ile	Tyr	Asp				
20																	55 60 65			
	ttc	att	ggg	gag	ttc	atg	aag	gcc	agc	gtg	gat	gtg	gca	gac	ctg	ata		356		
	Phe	Ile	Gly	Glu	Phe	Met	Lys	Ala	Ser	Val	Asp	Val	Ala	Asp	Leu	Ile				
																	70 75 80			
	ggc	cta	aac	ctt	gtc	atg	tcc	cgg	aat	gcc	ggc	aag	gga	gag	tac	aag		404		
25	Gly	Leu	Asn	Leu	Val	Met	Ser	Arg	Asn	Ala	Gly	Lys	Gly	Glu	Tyr	Lys				
																	85 90 95			
	atc	atg	gtt	gct	gcc	ctg	ggc	tgg	gcc	act	gct	gag	ctt	att	atg	tcc		452		
	Ile	Met	Val	Ala	Ala	Leu	Gly	Trp	Ala	Thr	Ala	Glu	Leu	Ile	Met	Ser				
																	100 105 110			
30	cgc	tgc	att	ccc	cta	tgg	gtc	gga	gcc	cgg	ggc	att	gag	ttt	gac	tgg		500		
	Arg	Cys	Ile	Pro	Leu	Trp	Val	Gly	Ala	Arg	Gly	Ile	Glu	Phe	Asp	Trp				
																	115 120 125 130			
	aag	tac	atc	cag	atg	agc	ata	gac	tcc	aac	atc	agt	ctg	gtc	cat	tac		548		
	Lys	Tyr	Ile	Gln	Met	Ser	Ile	Asp	Ser	Asn	Ile	Ser	Leu	Val	His	Tyr				
35																	135 140 145			

167/177

atc gtc gcg tct gct cag gtc tgg atg ata aca cgc tat gat ctg tac 596
 Ile Val Ala Ser Ala Gln Val Trp Met Ile Thr Arg Tyr Asp Leu Tyr
 150 155 160
 cac acc ttc cgg cca gct gtc ctc ctg ctg atg ttc ctc agt gtc tac 644
 5 His Thr Phe Arg Pro Ala Val Leu Leu Met Phe Leu Ser Val Tyr
 165 170 175
 aag gcc ttt gtt atg gag acc ttc gtc cac ctc tgc tcg ctg ggc agt 692
 Lys Ala Phe Val Met Glu Thr Phe Val His Leu Cys Ser Leu Gly Ser
 180 185 190
 10 tgg gca gct cta ctg gcc cga gca gtg gta acg ggg ctg ctg gcc ctc 740
 Trp Ala Ala Leu Leu Ala Arg Ala Val Val Thr Gly Leu Leu Ala Leu
 195 200 205 210
 agc act ttg gcc ctg tat gtc gcc gtt gtc aat gtg cac tcc taggett 790
 Ser Thr Leu Ala Leu Tyr Val Ala Val Val Asn Val His Ser
 15 215 220
 gtgtctcaga cattgatgta ccttttccct gcctcgctcc aggttttagt gaagtaaaca 850
 gtatttggaag agtt 864

 <210> 146
 20 <211> 1527
 <212> DNA
 <213> Homo sapience
 <220>
 <221> CDS
 25 <222> (25)...(801)

 <400> 146
 gcagtggccg ttacggccga aaag atg gcg gtc ttg gca cct cta att gct 51
 Met Ala Val Leu Ala Pro Leu Ile Ala
 30 1 5
 ctc gtg tat tcg gtg ccg cga ctt tca cga tgg ctc gcc caa cct tac 99
 Leu Val Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr
 10 15 20 25
 tac ctt ctg tcg gcc ctg ctc tct gct gcc ttc cta ctc gtg agg aaa 147
 35 Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys

168/177

	30	35	40	
	ctg ccg ccg ctc tgc cac ggt ctg ccc acc caa cgc gaa gac ggt aac			195
	Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn			
	45	50	55	
5	ccg tgt gac ttt gac tgg aga gaa gtg gag atc ctg atg ttt ctc agt			243
	Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser			
	60	65	70	
	gcc att gtg atg atg aag aac cgc aga tcc atg ttc ctg atg acg tgc			291
	Ala Ile Val Met Met Lys Asn Arg Arg Ser Met Phe Leu Met Thr Cys			
10	75	80	85	
	aaa ccc ccc cta tat atg ggc cct gag tat atc aag tac ttc aat gat			339
	Lys Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp			
	90	95	100	105
	aaa acc att gat gag gaa cta gaa cgg gac aag agg gtc act tgg att			387
15	Lys Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile			
	110	115	120	
	gtg gag ttc ttt gcc aat tgg tct aat gac tgc caa tca ttt gcc cct			435
	Val Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro			
	125	130	135	
20	atc tat gct gac ctc tcc ctt aaa tac aac tgt aca ggg cta aat ttt			483
	Ile Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe			
	140	145	150	
	ggg aag gtg gat gtt gga cgc tat act gat gtt agt acg cgg tac aaa			531
	Gly Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys			
25	155	160	165	
	gtg agc aca tca ccc ctc acc aag caa ctc cct acc ctg atc ctg ttc			579
	Val Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe			
	170	175	180	185
	caa ggt ggc aag gag gca atg cgg cgg cca cag att gac aag aaa gga			627
30	Gln Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly			
	190	195	200	
	cgg gct gtc tca tgg acc ttc tct gag gag aat gtg atc cga gaa ttt			675
	Arg Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe			
	205	210	215	
35	aac tta aat gag cta tac cag cgg gcc aag aaa cta tca aag gct gga			723

169/177

Asn Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly
 220 225 230
 gac aat atc cct gag gag cag cct gtg gct tca acc ccc acc aca gtg 771
 Asp Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val
 5 235 240 245
 tca gat ggg gaa aac aag aag gat aaa taagatcctc ac 810
 Ser Asp Gly Glu Asn Lys Lys Asp Lys
 250 255
 10 tttggcagtg cttcctctcc tgtcaattcc aggctctttc cataaccaca agcctgaggc 870
 tgcagccttt tatttatgtt ttccctttgg ctgtgactgg gtggggcagc atgcagcttc 930
 tgatttttaa gaggcata ggggaattgtc aggcacccta caggaaggcc tgccatgctg 990
 tggccaactg tttcactgga gcaagaaaga gatctcatag gacggagggg gaaatggttt 1050
 cctccaagc ttgggtcagt gtgttaactg cttatcagct attcagacat ctccatggtt 1110
 tctccatgaa actctgtggt ttcattcattc cttcttagtt gacctgcaca gcttggttag 1170
 15 acctagattt aaccctaagg taagatgctg gggatatagaa cgctaagaat tttcccccaa 1230
 ggactcttgc ttccttaagc cttctgtggt tcgtttatgg tcttcattaa aagtataagc 1290
 ctaactttgt cgctagtctt aaggagaaac ctttaaccac aaagttttta tcattgaaga 1350
 caatattgaa caaccccta ttttgtggg attgagaagg ggtgaataga ggcttgagac 1410
 tttcctttgt gtggtaggac ttggaggaga aatcccctgg actttcacta accctctgac 1470
 20 atactcccca caccagttg atggctttcc gtaataaaaa gattgggatt tcctttt 1527

 <210> 147
 <211> 659
 <212> DNA
 25 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (138)...(470)

 30 <400> 147
 agtcttccga gcaagatggc gccgcgggca tttcttccac tgcccgtctg agggaaacgt 60
 aagtagtggt tccggcgccg tgttccagct ccgctgtgtt ccgcgagaaa gcgagaggcc 120
 gagcccgggc tgggtgcg atg gcc gcg gtg gtg gcc aag cgg gaa ggg ccg 170
 Met Ala Ala Val Val Ala Lys Arg Glu Gly Pro
 35 1 5 10

170/177

ccg ttc atc agc gag gcg gcc gtg cgg ggc aac gcc gcc gtc ctg gat 218
 Pro Phe Ile Ser Glu Ala Ala Val Arg Gly Asn Ala Ala Val Leu Asp
 15 20 25
 tat tgc cgg acc tcg gtg tca gcg ctg tcg ggg gcc acg gcc ggc atc 266
 5 Tyr Cys Arg Thr Ser Val Ser Ala Leu Ser Gly Ala Thr Ala Gly Ile
 30 35 40
 ctc ggc ctc acc ggc ctc tac ggc ttc atc ttc tac ctg ctc gcc tcc 314
 Leu Gly Leu Thr Gly Leu Tyr Gly Phe Ile Phe Tyr Leu Leu Ala Ser
 45 50 55
 10 gtc ctg ctc tcc ctg ctc ctc att ctc aag gcg gga agg agg tgg aac 362
 Val Leu Leu Ser Leu Leu Leu Ile Leu Lys Ala Gly Arg Arg Trp Asn
 60 65 70 75
 aaa tat ttc aaa tca cgg aga cct ctc ttt aca gga ggc ctc atc ggg 410
 Lys Tyr Phe Lys Ser Arg Arg Pro Leu Phe Thr Gly Gly Leu Ile Gly
 15 80 85 90
 ggc ctc ttc acc tac gtc ctg ttc tgg acg ttc ctc tac ggc atg gtg 458
 Gly Leu Phe Thr Tyr Val Leu Phe Trp Thr Phe Leu Tyr Gly Met Val
 95 100 105
 cac gtc tac tgaaatgggg gcccggggga cttttttaaa aaa 500
 20 His Val Tyr
 110
 ccagatcggg aggactgtgg ccagcaatta acaccatgta gacttcctta gttcttaagt 560
 ggttgaattc gctgcttggt ctgtaacgtt ataaataatt tatatctgaa gacggagagc 620
 ctgtaatat cttcagatta aatgaagcgt gagacactt 659
 25
 <210> 148
 <211> 710
 <212> DNA
 <213> Homo sapience
 30 <220>
 <221> CDS
 <222> (68)...(343)
 <400> 148
 35 agaggggagat acagaaaccg acagggggcca ggcgcccggg ggctccgaag cggggaagtg 60

171/177

	ggacaag atg gtt tac atc tcg aac gga caa gtg ttg gac agc cgg agt	109
	Met Val Tyr Ile Ser Asn Gly Gln Val Leu Asp Ser Arg Ser	
	1 5 10	
5	cag tct cca tgg aga tta tct ttg ata aca gat ttc ttc tgg gga ata	157
	Gln Ser Pro Trp Arg Leu Ser Leu Ile Thr Asp Phe Phe Trp Gly Ile	
	15 20 25 30	
	gct gag ttt gtg gtt ttg ttt ttc aaa act ctg ctt cag caa gat gtg	205
	Ala Glu Phe Val Val Leu Phe Phe Lys Thr Leu Leu Gln Gln Asp Val	
	35 40 45	
10	aaa aaa aga aga agc tat gga aac tca tct gat tcc aga tat gat gat	253
	Lys Lys Arg Arg Ser Tyr Gly Asn Ser Ser Asp Ser Arg Tyr Asp Asp	
	50 55 60	
	gga aga ggg cca cca gga aac cct ccc cga aga atg ggt aga atc aat	301
	Gly Arg Gly Pro Pro Gly Asn Pro Pro Arg Arg Met Gly Arg Ile Asn	
15	65 70 75	
	cat ctg cgt ggc cct agt ccc cct cca atg gct ggt gga tgaggaaggt	350
	His Leu Arg Gly Pro Ser Pro Pro Pro Met Ala Gly Gly	
	80 85 90	
20	aaatgtctgc tctaagaagc agacaaccgg acatgcgcat tcatagcaga aggaaaccat	410
	caagaagtgg aaggctgacc atgatgagca gtagatgaat gtgtatgtct aaacaaggac	470
	tgctctgtgt cctcacagat gaatgaggtc atgctgggaa ttccctctgc agggaaactgg	530
	cctgactgac atgcagttcc ataaatgcag atgtttgtct cattaccttt ttgtatagtt	590
	tattaaagta ttaatatagt ttaataaagt aaatatTTTT aggttgcaga atggactcct	650
	catctttata ttcacgaaaa agcaatctga agaaaacaaa taaaagcctg tgtatttagc	710
25		
	<210> 149	
	<211> 2182	
	<212> DNA	
	<213> Homo sapience	
30	<220>	
	<221> CDS	
	<222> (56)...(1090)	
	<400> 149	
35	gcaettcagc ttccctccc ccggcgccct ctggggctcc gagcccggcg ggacc	58

172/177

	atg ttc acc agc acc ggc tcc agt ggg ctc tac aag gcg cct ctg tcg	103
	Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser	
	1 5 10 15	
5	aag agc ctt ctg ctg gtc ccc agt gcc ctc tcc ctc ctg ctc gcc ctc	151
	Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu	
	20 25 30	
	ctc ctg cct cac tgc cag aag ctc ttt gtg tat gac ctt cac gca gtc	199
	Leu Leu Pro His Cys Gln Lys Leu Phe Val Tyr Asp Leu His Ala Val	
	35 40 45	
10	aag aac gac ttc cag att tgg agg ttg ata tgt gga aga ata att tgc	247
	Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys	
	50 55 60	
	ctt gat ttg aaa gat act ttc tgc agt agt ctg ctt att tat aat ttt	295
	Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe	
15	65 70 75 80	
	agg ata ttt gaa aga aga tat gga agc aga aaa ttt gca tcc ttt ttg	343
	Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu	
	85 90 95	
	ctg ggt tcc tgg gtt ttg tca gcc tta ttt gac ttt ctc ctc att gaa	391
20	Leu Gly Ser Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu	
	100 105 110	
	gct atg cag tat ttc ttt ggc atc act gca gct agt aat ttg cct tct	439
	Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser	
	115 120 125	
25	gga ttc ctg gca cct gtg ttt gct ctg ttt gta cca ttt tac tgc tcc	487
	Gly Phe Leu Ala Pro Val Phe Ala Leu Phe Val Pro Phe Tyr Cys Ser	
	130 135 140	
	ata cca aga gtc caa gtg gca caa att ctg ggt ccg ttg tcc atc aca	535
	Ile Pro Arg Val Gln Val Ala Gln Ile Leu Gly Pro Leu Ser Ile Thr	
30	145 150 155 160	
	aac aag aca ttg att tat ata ttg gga ctg cag ctt ttc acc tct ggt	583
	Asn Lys Thr Leu Ile Tyr Ile Leu Gly Leu Gln Leu Phe Thr Ser Gly	
	165 170 175	
	tcc tac atc tgg att gta gcc ata agt gga ctt atg tcc ggt ctg tgc	631
35	Ser Tyr Ile Trp Ile Val Ala Ile Ser Gly Leu Met Ser Gly Leu Cys	

173/177

	180	185	190	
	tac gac agc aaa atg ttc cag gtg cat cag gtg ctc tgc atc ccc agc	679		
	Tyr Asp Ser Lys Met Phe Gln Val His Gln Val Leu Cys Ile Pro Ser			
	195	200	205	
5	tgg atg gca aaa ttc ttt tct tgg aca ctt gaa ccc atc ttc tct tct	727		
	Trp Met Ala Lys Phe Phe Ser Trp Thr Leu Glu Pro Ile Phe Ser Ser			
	210	215	220	
	tca gaa ccc acc agc gaa gcc aga att ggg atg gga gcc acg ctg gac	775		
	Ser Glu Pro Thr Ser Glu Ala Arg Ile Gly Met Gly Ala Thr Leu Asp			
10	225	230	235	240
	atc cag aga cag cag aga atg gag ctg ctg gac cgg cag ctg atg ttc	823		
	Ile Gln Arg Gln Gln Arg Met Glu Leu Leu Asp Arg Gln Leu Met Phe			
	245	250	255	
	tct cag ttt gca caa ggg agg cga cag aga cag cag cag gga gga atg	871		
15	Ser Gln Phe Ala Gln Gly Arg Arg Gln Arg Gln Gln Gln Gly Gly Met			
	260	265	270	
	atc aat tgg aat cgt ctt ttt cct cct tta cgt cag cga caa aac gta	919		
	Ile Asn Trp Asn Arg Leu Phe Pro Pro Leu Arg Gln Arg Gln Asn Val			
	275	280	285	
20	aac tat cag ggc ggt cgg cag tct gag cca gca gcg ccc cct cta gaa	967		
	Asn Tyr Gln Gly Gly Arg Gln Ser Glu Pro Ala Ala Pro Pro Leu Glu			
	290	295	300	
	gtt tct gag gaa cag gtc gcc cgg ctc atg gag atg gga ttt tcc aga	1015		
	Val Ser Glu Glu Gln Val Ala Arg Leu Met Glu Met Gly Phe Ser Arg			
25	305	310	315	320
	ggt gat gct ttg gaa gcc ctg aga gct tca aac aat gac ctc aat gtc	1063		
	Gly Asp Ala Leu Glu Ala Leu Arg Ala Ser Asn Asn Asp Leu Asn Val			
	325	330	335	
	gcc acc aac ttc ctg ctg cag cac tgatagtccc aggccaacac tgg	1110		
30	Ala Thr Asn Phe Leu Leu Gln His			
	340			
	gaccggaccg gcagccgagt gacagtgcgt ggtecccacc atcagatcag cccggggacc	1170		
	gagcatctct ggtgctgatg ttcttgtggg aagagggagg ttccaccgca cccctgccet	1230		
	caaccgcaag actgttgccg ttttagtggt gagataagtt tgccattaca ttagcatgta	1290		
35	ttttctatct atatttttta ttgggcattt tccctagggt ggagagtcag cactcgtttt	1350		

174/177

	gaatgtgttt aaaatgcatt aaaatggaag atttctgcag gcagttgaat ggcactccag	1410
	atggggaatt gctgtaaccc tcttactgta acatgtcatc tcctgcgtcg tgatggggag	1470
	agggtaaatgt tacttcacaa aggacatgtc agatccttct tcatggactt ttttagttac	1530
	tgttttttct ctcaaacttg ttttcgaatc tcctgggagt gagggagaaa caggagactg	1590
5	aatcctcccc caagctgttc caggccagag gactctgcag taccttctcc tacatctagt	1650
	aacaaagaat ggtgataacc atgcactggg tcaaggttct ggagttctcc atgaaacttg	1710
	ggtaattttt gctcagagta tccggagtta gccactaggc tgcgggtgaa atgggatgga	1770
	gtagaacaac agcaggcttc ctggagccac atgggctgac tagggcactc tgtggtggc	1830
	ctggcacggg ctccagcccag gaagaggaga aacgatccct tgctgcccc tccctgtggc	1890
10	agggctaact gcctggccct cctggctcgc agccagccag cccctggca gcaggttctc	1950
	ctcagggtt gggtcttcaa cctgtggcga caggaggcag ggcagactgt ggaggacagg	2010
	atgcaggtea gggagagggg aggcaggggg ggaccgccat gagcatgaaa agaccogaag	2070
	caagttgact cttgcaatgt gcaactgtta tgttctgcaa aatgagcaac gatgtatcaa	2130
	attgatgcaa atttagatgt tgatacttac aataaagttt ttaatgtgtt tt	2182
15	<210> 150	
	<211> 2773	
	<212> DNA	
	<213> Homo sapience	
20	<220>	
	<221> CDS	
	<222> (211)...(1497)	
	<400> 150	
25	gtagcggaga agactggagc tccgaggagc tgcactctgcg gcaacctgtg tgctgacgct	60
	acgtgcctcc tggtcccgac gtagctcgca gctccccagt ctcactccat tccttcccca	120
	cctggcgcgc acctgctcaa gaccagggtc ctgccaaagc ctaggagggc gcgtgccagg	180
	ggcgctaggg aactgaggag cgcgcgcgcc atg ggg ccg ccg cct ggg gcc	231
	Met Gly Pro Pro Pro Gly Ala	
30	1 5	
	ggg gtc tcc tgc cgc ggt ggc tgc ggc ttt tcc aga ttg ctg gca tgg	279
	Gly Val Ser Cys Arg Gly Gly Cys Gly Phe Ser Arg Leu Leu Ala Trp	
	10 15 20	
	tgc ttc ctg ctg gcc ctg agt ccg cag gca ccc ggt tcc cgg ggg gct	327
35	Cys Phe Leu Leu Ala Leu Ser Pro Gln Ala Pro Gly Ser Arg Gly Ala	

175/177

	25	30	35	
	gaa gca gtg tgg acc gcg tac ctc aac gtg tcc tgg cgg gtt ccg cac			375
	Glu Ala Val Trp Thr Ala Tyr Leu Asn Val Ser Trp Arg Val Pro His			
	40	45	50	55
5	acg gga gtg aac cgt acg gtg tgg gag ctg agc gag gag ggc gtg tac			423
	Thr Gly Val Asn Arg Thr Val Trp Glu Leu Ser Glu Glu Gly Val Tyr			
	60	65	70	
	ggc cag gac tgg ccg ctg gag cct gtg gct ggg gtc ctg gta ccg ccc			471
	Gly Gln Asp Ser Pro Leu Glu Pro Val Ala Gly Val Leu Val Pro Pro			
10	75	80	85	
	gac ggg ccc ggg gcg ctt aac gcc tgt aac ccg cac acg aat ttc acg			519
	Asp Gly Pro Gly Ala Leu Asn Ala Cys Asn Pro His Thr Asn Phe Thr			
	90	95	100	
	gtg ccc acg gtt tgg gga agc acc gtg caa gtc tct tgg ttg gcc ctc			567
15	Val Pro Thr Val Trp Gly Ser Thr Val Gln Val Ser Trp Leu Ala Leu			
	105	110	115	
	atc caa cgc ggc ggg ggc tgc acc ttc gca gac aag atc cat ctg gct			615
	Ile Gln Arg Gly Gly Gly Cys Thr Phe Ala Asp Lys Ile His Leu Ala			
	120	125	130	135
20	tat gag aga ggg gcg tct gga gcc gtc atc ttt aac ttc ccc ggg acc			663
	Tyr Glu Arg Gly Ala Ser Gly Ala Val Ile Phe Asn Phe Pro Gly Thr			
	140	145	150	
	cgc aat gag gtc atc ccc atg tct cac ccg ggt gca gta gac att gtt			711
	Arg Asn Glu Val Ile Pro Met Ser His Pro Gly Ala Val Asp Ile Val			
25	155	160	165	
	gca atc atg atc ggc aat ctg aaa ggc aca aaa att ctg caa tct att			759
	Ala Ile Met Ile Gly Asn Leu Lys Gly Thr Lys Ile Leu Gln Ser Ile			
	170	175	180	
	caa aga ggc ata caa gtg aca atg gtc ata gaa gta ggg aaa aaa cat			807
30	Gln Arg Gly Ile Gln Val Thr Met Val Ile Glu Val Gly Lys Lys His			
	185	190	195	
	ggc cct tgg gtg aat cac tat tca att ttt ttc gtt tct gtg tcc ttt			855
	Gly Pro Trp Val Asn His Tyr Ser Ile Phe Phe Val Ser Val Ser Phe			
	200	205	210	215
35	ttt att att acg gcg gca act gtg ggc tat ttt atc ttt tat tct gct			903

176/177

	Phe Ile Ile Thr Ala Ala Thr Val Gly Tyr Phe Ile Phe Tyr Ser Ala	
	220 225 230	
	cga agg cta cgg aat gca aga gct caa agc agg aag cag agg caa tta	951
	Arg Arg Leu Arg Asn Ala Arg Ala Gln Ser Arg Lys Gln Arg Gln Leu	
5	235 240 245	
	aag gca gat gct aaa aaa gct att gga agg ctt caa cta cgc aca ctg	999
	Lys Ala Asp Ala Lys Lys Ala Ile Gly Arg Leu Gln Leu Arg Thr Leu	
	250 255 260	
	aaa caa gga gac aag gaa att ggc cct gat gga gat agt tgt gct gtg	1047
10	Lys Gln Gly Asp Lys Glu Ile Gly Pro Asp Gly Asp Ser Cys Ala Val	
	265 270 275	
	tgc att gaa ttg tat aaa cca aat gat ttg gta cgc atc tta acg tgc	1095
	Cys Ile Glu Leu Tyr Lys Pro Asn Asp Leu Val Arg Ile Leu Thr Cys	
	280 285 290 295	
15	aac cat att ttc cat aag aca tgt gtt gac cca tgg ctg tta gaa cac	1143
	Asn His Ile Phe His Lys Thr Cys Val Asp Pro Trp Leu Leu Glu His	
	300 305 310	
	agg act tgc ccc atg tgc aaa tgt gac ata ctc aaa gct ttg gga att	1191
	Arg Thr Cys Pro Met Cys Lys Cys Asp Ile Leu Lys Ala Leu Gly Ile	
20	315 320 325	
	gag gtg gat gtt gaa gat gga tca gtg tct tta caa gtc cct gta tcc	1239
	Glu Val Asp Val Glu Asp Gly Ser Val Ser Leu Gln Val Pro Val Ser	
	330 335 340	
	aat gaa ata tct aat agt gcc tcc tcc cat gaa gag gat aat cgc agc	1287
25	Asn Glu Ile Ser Asn Ser Ala Ser Ser His Glu Glu Asp Asn Arg Ser	
	345 350 355	
	gag acc gca tca tct gga tat gct tca gta cag gga aca gat gaa ccg	1335
	Glu Thr Ala Ser Ser Gly Tyr Ala Ser Val Gln Gly Thr Asp Glu Pro	
	360 365 370 375	
30	cct ctg gag gaa cac gtg cag tca aca aat gaa agt cta cag ctg gta	1383
	Pro Leu Glu Glu His Val Gln Ser Thr Asn Glu Ser Leu Gln Leu Val	
	380 385 390	
	aac cat gaa gca aat tct gtg gca gtg gat gtt att cct cat gtt gac	1431
	Asn His Glu Ala Asn Ser Val Ala Val Asp Val Ile Pro His Val Asp	
35	395 400 405	

177/177

	aac cca acc ttt gaa gaa gac gaa act cct aat caa gag act gct gtt	1479
	Asn Pro Thr Phe Glu Glu Asp Glu Thr Pro Asn Gln Glu Thr Ala Val	
	410 415 420	
	cga gaa att aaa tct taaaatctgt gtaaatagaa aacttgaacc attagt	1530
5	Arg Glu Ile Lys Ser	
	425	
	aataacagaa ctgccaatca gggcctagtt tctattaata aattggataa atttaataaa	1590
	ataagagtga tactgaaagt gctcagatga ctaatattat gctatagtta aatggcttaa	1650
	aatattttaac ctgttaactt tttccacaa actcattata atatttttca taggcaagtt	1710
10	tcctctcagt agtgataaca acatttttag acattcaaaa ctgtcttcaa gaagtcacgt	1770
	ttttcattta taacaatttt cttataaaaa catgttgctt ttaaaatgtg gagtagctgt	1830
	aatcacttta ttttatgata gtatcttaat gaaaaatact acttctttag cttgggctac	1890
	atgtgtcagg gtttttctcc aggtgcttat attgatctgg aattgtaatg taaaaagcaa	1950
	tgcaaaactta ggcgagtact tcttgaaatg tctattttaag ctgctttaag ttaatagaaa	2010
15	agattaaagc aaaatattca tttttacttt ttcttatttt taaaattagg ctgaatgtac	2070
	ttcatgtgat ttgtcaacca tagtttatca gagattatgg acttaattga ttggtatatt	2130
	agtgacatca acttgacaca agattagaca aaaaattcct tacaaaaata ctgtgtaact	2190
	atctctcaaaa cttgtgggat ttttcaaaaag ctgagtatat gaatcatcat actgtttgaa	2250
	attgctaattg acagagtaag taacactaat attggtcatt gatcttcggt catgaattag	2310
20	tctacagaaa aaaaatgttc tgtaaaatta gtctgttgaa aatgttttcc aaacaatgtt	2370
	actttgaaaa ttgagtttat gtttgaccta aatgggctaa aattatatta gataaactaa	2430
	aattctgtcc gtgtaactat aaattttgtg aatgcatttt cctgggtgtt gaaaaagaag	2490
	ggggggagaa ttccaggtgc cttaatatata agtttgaagc ttcacccacc aaagttaa	2550
	agagctatctt aaaaatgcac tttatttgta ctctgtgtgg cttttgtttt agaattttgt	2610
25	tcaaattata gcagaattta ggcaaaaata aaacagacat gtatttttgt ttgctgaatg	2670
	gatgaaacca ttgcattctt gtacactgat ttgaaatgct gtaaataatgt cccaatttgt	2730
	attgattctc tttaaatata aaatgtaaat aaaatattcc aat	2773